

# SEQUENCE LISTING

RECEIVED  
TECH CENTER 1600/2300  
01 DEC 20 PM 12:48

<110> Zuker, Charles S.  
Ryba, Nicholas J.P.  
Nelson, Greg  
Hoon, Mark A.  
Chandrashekar, Jayaram  
Zhang, Yifeng  
The Regents of the University of California  
The Government of the United States of America  
as represented by the Secretary of the  
Department of Health and Human Services

<120> Mammalian Sweet Taste Receptors

<130> 02307E-120110US

<140> US 09/927,315

<141> 2001-08-10

<150> US 60/302,898

<151> 2001-07-03

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 840

<212> PRT

<213> Rattus sp.

<220>

<223> rat T1R1 sweet taste receptor

<400> 1

Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Val Tyr  
1 5 10 15

Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly Phe Ser  
20 25 30

Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His Gly Asp  
35 40 45

Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp Arg Pro  
50 55 60

Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg Phe  
65 70 75 80

Thr Val Glu Glu Ile Asn Asn Ser Ser Ala Leu Leu Pro Asn Ile Thr  
85 90 95

Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val Tyr  
100 105 110

Ala Thr Leu Arg Val Leu Ala Leu Gln Gly Pro Arg His Ile Glu Ile  
115 120 125

Gln	Lys	Asp	Leu	Arg	Asn	His	Ser	Ser	Lys	Val	Val	Ala	Phe	Ile	Gly	
130						135					140					
Pro	Asp	Asn	Thr	Asp	His	Ala	Val	Thr	Thr	Ala	Ala	Leu	Leu	Gly	Pro	
145					150					155					160	
Phe	Leu	Met	Pro	Leu	Val	Ser	Tyr	Glu	Ala	Ser	Ser	Val	Val	Leu	Ser	
				165					170					175		
Ala	Lys	Arg	Lys	Phe	Pro	Ser	Phe	Leu	Arg	Thr	Val	Pro	Ser	Asp	Arg	
			180					185					190			
His	Gln	Val	Glu	Val	Met	Val	Gln	Leu	Leu	Gln	Ser	Phe	Gly	Trp	Val	
	195						200					205				
Trp	Ile	Ser	Leu	Ile	Gly	Ser	Tyr	Gly	Asp	Tyr	Gly	Gln	Leu	Gly	Val	
	210					215					220					
Gln	Ala	Leu	Glu	Glu	Leu	Ala	Val	Pro	Arg	Gly	Ile	Cys	Val	Ala	Phe	
225					230					235					240	
Lys	Asp	Ile	Val	Pro	Phe	Ser	Ala	Arg	Val	Gly	Asp	Pro	Arg	Met	Gln	
				245					250					255		
Ser	Met	Met	Gln	His	Leu	Ala	Gln	Ala	Arg	Thr	Thr	Val	Val	Val	Val	
			260					265					270			
Phe	Ser	Asn	Arg	His	Leu	Ala	Arg	Val	Phe	Phe	Arg	Ser	Val	Val	Leu	
		275					280					285				
Ala	Asn	Leu	Thr	Gly	Lys	Val	Trp	Val	Ala	Ser	Glu	Asp	Trp	Ala	Ile	
	290					295					300					
Ser	Thr	Tyr	Ile	Thr	Ser	Val	Thr	Gly	Ile	Gln	Gly	Ile	Gly	Thr	Val	
305					310					315					320	
Leu	Gly	Val	Ala	Val	Gln	Gln	Arg	Gln	Val	Pro	Gly	Leu	Lys	Glu	Phe	
				325					330					335		
Glu	Glu	Ser	Tyr	Val	Arg	Ala	Val	Thr	Ala	Ala	Pro	Ser	Ala	Cys	Pro	
			340					345					350			
Glu	Gly	Ser	Trp	Cys	Ser	Thr	Asn	Gln	Leu	Cys	Arg	Glu	Cys	His	Thr	
		355					360					365				
Phe	Thr	Thr	Arg	Asn	Met	Pro	Thr	Leu	Gly	Ala	Phe	Ser	Met	Ser	Ala	
	370					375					380					
Ala	Tyr	Arg	Val	Tyr	Glu	Ala	Val	Tyr	Ala	Val	Ala	His	Gly	Leu	His	
385					390					395					400	
Gln	Leu	Leu	Gly	Cys	Thr	Ser	Glu	Ile	Cys	Ser	Arg	Gly	Pro	Val	Tyr	
				405					410					415		
Pro	Trp	Gln	Leu	Leu	Gln	Gln	Ile	Tyr	Lys	Val	Asn	Phe	Leu	Leu	His	
		420						425					430			
Glu	Asn	Thr	Val	Ala	Phe	Asp	Asp	Asn	Gly	Asp	Thr	Leu	Gly	Tyr	Tyr	
	435						440					445				

Asp	Ile	Ile	Ala	Trp	Asp	Trp	Asn	Gly	Pro	Glu	Trp	Thr	Phe	Glu	Ile	450	455	460	
Ile	Gly	Ser	Ala	Ser	Leu	Ser	Pro	Val	His	Leu	Asp	Ile	Asn	Lys	Thr	465	470	475	480
Lys	Ile	Gln	Trp	His	Gly	Lys	Asn	Asn	Gln	Val	Pro	Val	Ser	Val	Cys	485	490	495	
Thr	Thr	Asp	Cys	Leu	Ala	Gly	His	His	Arg	Val	Val	Val	Gly	Ser	His	500	505	510	
His	Cys	Cys	Phe	Glu	Cys	Val	Pro	Cys	Glu	Ala	Gly	Thr	Phe	Leu	Asn	515	520	525	
Met	Ser	Glu	Leu	His	Ile	Cys	Gln	Pro	Cys	Gly	Thr	Glu	Glu	Trp	Ala	530	535	540	
Pro	Lys	Glu	Ser	Thr	Thr	Cys	Phe	Pro	Arg	Thr	Val	Glu	Phe	Leu	Ala	545	550	555	560
Trp	His	Glu	Pro	Ile	Ser	Leu	Val	Leu	Ile	Ala	Ala	Asn	Thr	Leu	Leu	565	570	575	
Leu	Leu	Leu	Leu	Val	Gly	Thr	Ala	Gly	Leu	Phe	Ala	Trp	His	Phe	His	580	585	590	
Thr	Pro	Val	Val	Arg	Ser	Ala	Gly	Gly	Arg	Leu	Cys	Phe	Leu	Met	Leu	595	600	605	
Gly	Ser	Leu	Val	Ala	Gly	Ser	Cys	Ser	Phe	Tyr	Ser	Phe	Phe	Gly	Glu	610	615	620	
Pro	Thr	Val	Pro	Ala	Cys	Leu	Leu	Arg	Gln	Pro	Leu	Phe	Ser	Leu	Gly	625	630	635	640
Phe	Ala	Ile	Phe	Leu	Ser	Cys	Leu	Thr	Ile	Arg	Ser	Phe	Gln	Leu	Val	645	650	655	
Ile	Ile	Phe	Lys	Phe	Ser	Thr	Lys	Val	Pro	Thr	Phe	Tyr	Arg	Thr	Trp	660	665	670	
Ala	Gln	Asn	His	Gly	Ala	Gly	Leu	Phe	Val	Ile	Val	Ser	Ser	Thr	Val	675	680	685	
His	Leu	Leu	Ile	Cys	Leu	Thr	Trp	Leu	Val	Met	Trp	Thr	Pro	Arg	Pro	690	695	700	
Thr	Arg	Glu	Tyr	Gln	Arg	Phe	Pro	His	Leu	Val	Ile	Leu	Glu	Cys	Thr	705	710	715	720
Glu	Val	Asn	Ser	Val	Gly	Phe	Leu	Leu	Ala	Phe	Thr	His	Asn	Ile	Leu	725	730	735	
Leu	Ser	Ile	Ser	Thr	Phe	Val	Cys	Ser	Tyr	Leu	Gly	Lys	Glu	Leu	Pro	740	745	750	
Glu	Asn	Tyr	Asn	Glu	Ala	Lys	Cys	Val	Thr	Phe	Ser	Leu	Leu	Leu	Asn	755	760	765	

Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ala Ser Ile Tyr Gln Gly  
 770 775 780  
 Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Thr Thr Leu Ser  
 785 790 795 800  
 Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys  
 805 810 815  
 Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile Gln Asp  
 820 825 830  
 Tyr Thr Arg Arg Cys Gly Thr Thr  
 835 840

<210> 2  
 <211> 842  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> mouse T1R1 sweet taste receptor

<400> 2  
 Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Ala Val  
 1 5 10 15  
 Ala Tyr Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly  
 20 25 30  
 Phe Ser Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His  
 35 40 45  
 Ala Asp Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp  
 50 55 60  
 Arg Ser Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met  
 65 70 75 80  
 Arg Phe Thr Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn  
 85 90 95  
 Ile Thr Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ser Asn  
 100 105 110  
 Val Tyr Ala Thr Leu Arg Val Pro Ala Gln Gln Gly Thr Gly His Leu  
 115 120 125  
 Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu  
 130 135 140  
 Ile Gly Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu  
 145 150 155 160  
 Ser Pro Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Ile  
 165 170 175  
 Leu Ser Gly Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Ile Pro Ser  
 180 185 190

Asp	Lys	Tyr	Gln	Val	Glu	Val	Ile	Val	Arg	Leu	Leu	Gln	Ser	Phe	Gly	
		195					200					205				
Trp	Val	Trp	Ile	Ser	Leu	Val	Gly	Ser	Tyr	Gly	Asp	Tyr	Gly	Gln	Leu	
	210					215					220					
Gly	Val	Gln	Ala	Leu	Glu	Glu	Leu	Ala	Thr	Pro	Arg	Gly	Ile	Cys	Val	
225					230					235					240	
Ala	Phe	Lys	Asp	Val	Val	Pro	Leu	Ser	Ala	Gln	Ala	Gly	Asp	Pro	Arg	
			245						250					255		
Met	Gln	Arg	Met	Met	Leu	Arg	Leu	Ala	Arg	Ala	Arg	Thr	Thr	Val	Val	
			260					265						270		
Val	Val	Phe	Ser	Asn	Arg	His	Leu	Ala	Gly	Val	Phe	Phe	Arg	Ser	Val	
		275					280					285				
Val	Leu	Ala	Asn	Leu	Thr	Gly	Lys	Val	Trp	Ile	Ala	Ser	Glu	Asp	Trp	
	290					295					300					
Ala	Ile	Ser	Thr	Tyr	Ile	Thr	Asn	Val	Pro	Gly	Ile	Gln	Gly	Ile	Gly	
305					310					315					320	
Thr	Val	Leu	Gly	Val	Ala	Ile	Gln	Gln	Arg	Gln	Val	Pro	Gly	Leu	Lys	
			325						330					335		
Glu	Phe	Glu	Glu	Ser	Tyr	Val	Gln	Ala	Val	Met	Gly	Ala	Pro	Arg	Thr	
			340					345					350			
Cys	Pro	Glu	Gly	Ser	Trp	Cys	Gly	Thr	Asn	Gln	Leu	Cys	Arg	Glu	Cys	
		355					360					365				
His	Ala	Phe	Thr	Thr	Trp	Asn	Met	Pro	Glu	Leu	Gly	Ala	Phe	Ser	Met	
	370					375					380					
Ser	Ala	Ala	Tyr	Asn	Val	Tyr	Glu	Ala	Val	Tyr	Ala	Val	Ala	His	Gly	
385				390						395					400	
Leu	His	Gln	Leu	Leu	Gly	Cys	Thr	Ser	Gly	Thr	Cys	Ala	Arg	Gly	Pro	
			405						410					415		
Val	Tyr	Pro	Trp	Gln	Leu	Leu	Gln	Gln	Ile	Tyr	Lys	Val	Asn	Phe	Leu	
			420					425					430			
Leu	His	Lys	Lys	Thr	Val	Ala	Phe	Asp	Asp	Lys	Gly	Asp	Pro	Leu	Gly	
		435				440						445				
Tyr	Tyr	Asp	Ile	Ile	Ala	Trp	Asp	Trp	Asn	Gly	Pro	Glu	Trp	Thr	Phe	
	450					455					460					
Glu	Val	Ile	Gly	Ser	Ala	Ser	Leu	Ser	Pro	Val	His	Leu	Asp	Ile	Asn	
465					470					475					480	
Lys	Thr	Lys	Ile	Gln	Trp	His	Gly	Lys	Asn	Asn	Gln	Val	Pro	Val	Ser	
			485						490					495		
Val	Cys	Thr	Arg	Asp	Cys	Leu	Glu	Gly	His	His	Arg	Leu	Val	Met	Gly	
			500					505					510			

Ser His His Cys Cys Phe Glu Cys Met Pro Cys Glu Ala Gly Thr Phe  
 515 520 525  
 Leu Asn Thr Ser Glu Leu His Thr Cys Gln Pro Cys Gly Thr Glu Glu  
 530 535 540  
 Trp Ala Pro Glu Gly Ser Ser Ala Cys Phe Ser Arg Thr Val Glu Phe  
 545 550 555 560  
 Leu Gly Trp His Glu Pro Ile Ser Leu Val Leu Leu Ala Ala Asn Thr  
 565 570 575  
 Leu Leu Leu Leu Leu Leu Ile Gly Thr Ala Gly Leu Phe Ala Trp Arg  
 580 585 590  
 Leu His Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu  
 595 600 605  
 Met Leu Gly Ser Leu Val Ala Gly Ser Cys Ser Leu Tyr Ser Phe Phe  
 610 615 620  
 Gly Lys Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser  
 625 630 635 640  
 Leu Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln  
 645 650 655  
 Leu Val Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His  
 660 665 670  
 Thr Trp Ala Gln Asn His Gly Ala Gly Ile Phe Val Ile Val Ser Ser  
 675 680 685  
 Thr Val His Leu Phe Leu Cys Leu Thr Trp Leu Ala Met Trp Thr Pro  
 690 695 700  
 Arg Pro Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu  
 705 710 715 720  
 Cys Thr Glu Val Asn Ser Val Gly Phe Leu Val Ala Phe Ala His Asn  
 725 730 735  
 Ile Leu Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu  
 740 745 750  
 Leu Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu  
 755 760 765  
 Leu His Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ser Ser Ile Tyr  
 770 775 780  
 Gln Gly Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Ala Thr  
 785 790 795 800  
 Leu Ser Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile  
 805 810 815  
 Leu Cys Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile  
 820 825 830

Gln Asp Tyr Thr Arg Arg Cys Gly Thr Thr  
 835 840

<210> 3  
 <211> 777  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T1R1 sweet taste receptor

<400> 3  
 Arg Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met  
 1 5 10 15  
 Arg Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn  
 20 25 30  
 Ile Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn  
 35 40 45  
 Val Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile  
 50 55 60  
 Glu Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val  
 65 70 75 80  
 Ile Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu  
 85 90 95  
 Ser Pro Phe Leu Val His Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu  
 100 105 110  
 Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp  
 115 120 125  
 Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp  
 130 135 140  
 Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly  
 145 150 155 160  
 Val Gln Ala Leu Glu Asn Gln Ala Leu Val Arg Gly Ile Cys Ile Ala  
 165 170 175  
 Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met  
 180 185 190  
 Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val  
 195 200 205  
 Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val  
 210 215 220  
 Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala  
 225 230 235 240  
 Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met  
 245 250 255

Val	Leu	Gly	Val	Ala	Ile	Gln	Lys	Arg	Ala	Val	Pro	Gly	Leu	Lys	Ala	260	265	270
Phe	Glu	Glu	Ala	Tyr	Ala	Arg	Ala	Asp	Lys	Glu	Ala	Pro	Arg	Pro	Cys	275	280	285
His	Lys	Gly	Ser	Trp	Cys	Ser	Ser	Asn	Gln	Leu	Cys	Arg	Glu	Cys	Gln	290	295	300
Ala	Phe	Met	Ala	His	Thr	Met	Pro	Lys	Leu	Lys	Ala	Phe	Ser	Met	Ser	305	310	315
Ser	Ala	Tyr	Asn	Ala	Tyr	Arg	Ala	Val	Tyr	Ala	Val	Ala	His	Gly	Leu	325	330	335
His	Gln	Leu	Leu	Gly	Cys	Ala	Ser	Glu	Leu	Cys	Ser	Arg	Gly	Arg	Val	340	345	350
Tyr	Pro	Trp	Gln	Leu	Leu	Glu	Gln	Ile	His	Lys	Val	His	Phe	Leu	Leu	355	360	365
His	Lys	Asp	Thr	Val	Ala	Phe	Asn	Asp	Asn	Arg	Asp	Pro	Leu	Ser	Ser	370	375	380
Tyr	Asn	Ile	Ile	Ala	Trp	Asp	Trp	Asn	Gly	Pro	Lys	Trp	Thr	Phe	Thr	385	390	395
Val	Leu	Gly	Ser	Ser	Thr	Trp	Ser	Pro	Val	Gln	Leu	Asn	Ile	Asn	Glu	405	410	415
Thr	Lys	Ile	Gln	Trp	His	Gly	Lys	Asn	His	Gln	Val	Pro	Lys	Ser	Val	420	425	430
Cys	Ser	Ser	Asp	Cys	Leu	Glu	Gly	His	Gln	Arg	Val	Val	Thr	Gly	Phe	435	440	445
His	His	Cys	Cys	Phe	Glu	Cys	Val	Pro	Cys	Gly	Ala	Gly	Thr	Phe	Leu	450	455	460
Asn	Lys	Ser	Glu	Leu	Tyr	Arg	Cys	Gln	Pro	Cys	Gly	Thr	Glu	Glu	Trp	465	470	475
Ala	Pro	Glu	Gly	Ser	Gln	Thr	Cys	Phe	Pro	Arg	Thr	Val	Val	Phe	Leu	485	490	495
Ala	Leu	Arg	Glu	His	Thr	Ser	Trp	Val	Leu	Leu	Ala	Ala	Asn	Thr	Leu	500	505	510
Leu	Leu	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Gly	Leu	Phe	Ala	Trp	His	Leu	515	520	525
Asp	Thr	Pro	Val	Val	Arg	Ser	Ala	Gly	Gly	Arg	Leu	Cys	Phe	Leu	Met	530	535	540
Leu	Gly	Ser	Leu	Ala	Ala	Gly	Ser	Gly	Ser	Leu	Tyr	Gly	Phe	Phe	Gly	545	550	555
Glu	Pro	Thr	Arg	Pro	Ala	Cys	Leu	Leu	Arg	Gln	Ala	Leu	Phe	Ala	Leu	565	570	575



Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu  
 580 585 590  
 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala  
 595 600 605  
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala  
 610 615 620  
 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu  
 625 630 635 640  
 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys  
 645 650 655  
 Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly  
 660 665 670  
 Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu  
 675 680 685  
 Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe  
 690 695 700  
 Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp  
 705 710 715 720  
 Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu  
 725 730 735  
 Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu  
 740 745 750  
 Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln  
 755 760 765  
 Asp Tyr Thr Arg Arg Cys Gly Ser Thr  
 770 775

<210> 4  
 <211> 2771  
 <212> DNA  
 <213> Rattus sp.

<220>  
 <223> rat T1R1 sweet taste receptor

<400> 4  
 attcacatca gagctgtgct cagccatgct gggcagaggg acgacggctg gccagcatgc 60  
 tcttctgggc tgetcacctg ctgctcagcc tgcagttggt ctactgctgg gctttcagct 120  
 gccaaaggac agagtcctct ccaggttca gccttctctg ggacttcctc cttgcaggtc 180  
 tgttctccct ccatggtgac tgtctgcagg tgagacacag acctctggtg acaagttgtg 240  
 acaggcccga cagcttcaac ggccatggct accacctctt ccaagccatg cggttcactg 300  
 ttgaggagat aaacaactcc tcggccctgc ttcccaacat caccctgggg tatgagctgt 360  
 acgacgtgtg ctcagaatct gccaatgtgt atgccaccct gaggggtgctt gccctgcaag 420  
 ggccccgcca catagagata cagaaagacc ttgcgaacca ctctccaag gtggtggcct 480  
 tcatcgggcc tgacaacact gaccacgctg tcactaccgc tgccttgctg ggtcctttcc 540  
 tgatgccccct ggctcagctat gaggcaagca gcgtgggtact cagtgccaag cgcaagttcc 600  
 cgtcttttct tcgtaccgtc cccagtgcacc ggcaccaggt ggaggtcatg gtgcagctgc 660  
 tgcagagttt tgggtgggtg tggatctcgc tcattggcag ctacgggtgat tacgggcagc 720

tgggtgtgca	ggcgctggag	gagctggccg	tgccccgggg	catctgcgtc	gccttcaagg	780
acatcgtgcc	tttctctgcc	cgggtgggtg	acccgaggat	gcagagcatg	atgcagcatc	840
tggctcaggc	caggaccacc	gtggttgtgg	tcttctctaa	ccggcacctg	gctagagtgt	900
tcttcaggtc	cgtggtgctg	gccaacctga	ctggcaaaagt	gtgggtcgcc	tcagaagact	960
gggccaatctc	cacgtacatc	accagcgtga	ctgggatcca	aggcattggg	acgggtgctcg	1020
gtgtggccgt	ccagcagaga	caagtccttg	ggctgaagga	gtttgaggag	tcttatgtca	1080
gggctgtaac	agctgctccc	agcgttgcc	cggaggggtc	ctgggtgcagc	actaaccagc	1140
tgtgccggga	gtgccacacg	ttcacgactc	gtaacatgcc	cacgcttgga	gccttctcca	1200
tgagtgccgc	ctacagagtg	tatgaggctg	tgtacgctgt	ggccccacggc	ctccaccagc	1260
tcttgggatg	tacttctgag	atctgttcca	gaggcccagt	ctacccctgg	cagcttcttc	1320
agcagatcta	caaggtgaat	tttcttctac	atgagaatac	tgtggcattt	gatgacaacg	1380
gggacactct	agggtactac	gacatcatcg	cctgggactg	gaatggacct	gaatggacct	1440
ttgagatcat	tggctctgcc	tactgtcttc	cagttcatct	ggacataaat	aagacaaaaa	1500
tccagtggca	cgggaagaac	aatcagggtg	ctgtgtcagt	gtgtaccacg	gactgtctgg	1560
cagggcacca	cagggtgggt	gtgggttccc	accactgctg	ctttgagtgt	gtgccctgcg	1620
aagctgggac	ctttctcaac	atgagtgage	ttcacatctg	ccagccttgt	ggaacagaag	1680
aatgggcacc	caaggagagc	actacttgct	tcccacgcac	ggtggagtgc	ttggcttggc	1740
atgaacccat	ctctttgggtg	ctaatagcag	ctaacacgct	attgctgctg	ctgctgggtg	1800
ggactgctgg	cctgtttgcc	tggcattttc	acacacctgt	agtgagggtca	gctgggggta	1860
ggctgtgctt	cctcatgctg	ggttccttgg	tggccggaag	ttgcagcttc	tatagcttct	1920
tggggagcc	cacggtgccc	gcgtgcttgc	tgcgtcagcc	cctcttttct	ctcgggtttg	1980
ccatcttctc	ctcctgcctg	acaatccgct	ccttccaact	ggatcatcatc	ttcaagtttt	2040
ctaccaaggt	gcccacattc	taccgtacct	gggccccaaa	ccatggtgca	ggtctattcg	2100
tcattgtcag	ctccacgggtc	catttgcctc	tctgtctcac	atggcttgta	atgtggacct	2160
cacgaccac	cagggaatac	cagcgttccc	cccactctgg	gattctcgag	tgcacagagg	2220
tcaactctgt	aggcttctctg	ttggctttca	cccacaacat	tctcctctcc	atcagtacct	2280
tcgctctgcag	ctacctgggt	aaggaaactgc	cagagaacta	taatgaagcc	aaatgtgtca	2340
ccttcagcct	gctcctcaac	ttcgtatcct	ggatgcgctt	cttcaccatg	gccagcattt	2400
accagggcag	ctacctgcct	gcggtcaatg	tgctggcagg	gctgaccaca	ctgagcggcg	2460
gcttcagcgg	ttacttctct	cccaagtgtc	atgtgattct	ctgccgtcca	gaactcaaca	2520
atacagaaca	ctttcaggcc	tccatccagg	actacacgag	gcgctgcggc	actacctgat	2580
ccactggaaa	ggtgcagacg	ggaaggaagc	ctctcttctt	gtgctgaagg	tggcgggtcc	2640
agtggggccg	agagcttgag	gtgtctggga	gagctccggc	acagcttacg	atgtataagc	2700
acgcggaaga	atccagtgc	ataaagacgg	gaagtgtgaa	aaaaaaaaaa	aaaaaaaaaa	2760
aaaaaaaaaa	a					2771

<210> 5

<211> 2579

<212> DNA

<213> Mus musculus

<220>

<223> mouse T1R1 sweet taste receptor

<400> 5

tttgccagc	atgcttttct	gggcagctca	cctgctgctc	agcctgcagc	tggccgttgc	60
ttactgctgg	gctttcagct	gcccaggac	agaatcctct	ccaggtttca	gcttccctgg	120
ggacttctct	ctggcaggcc	tgttctccct	ccatgctgac	tgtctgcagg	tgagacacag	180
acctctggtg	acaagtgtgtg	acaggctctga	cagcttcaac	ggccatggct	atcacctctt	240
ccaagccatg	cggttcaccg	ttgaggagat	aaacaactcc	acagctctgc	ttcccaacat	300
caccttgggg	tatgaactgt	atgacgtgtg	ctcagagtct	tccaatgtct	atgccaccct	360
gagggtgccc	gcccagcaag	ggacaggcca	cctagagatg	cagagagatc	ttcgcaacca	420
ctcctccaag	gtggtggcac	tcattggggc	tgataaacact	gaccacgctg	tcaccactgc	480
tgcctgctg	agcccttttc	tgatgcccct	ggtcagctat	gaggcgagca	gcgtgatcct	540
cagtgggaag	cgcaagttcc	cgtecttctt	gcgcaccatc	cccagcgata	agtaccaggt	600
ggaagtcata	gtgcggctgc	tgcagagctt	cggctgggtc	tggatctcgc	tcgttggcag	660
ctatggtgac	tacgggcagc	tgggcgtaca	ggcgtgggag	gagctggcca	ctccacgggg	720
catctgcgtc	gccttcaagg	acgtggtgcc	tctctccgcc	caggcgggtg	acccaaggat	780
gcagcgcacg	atgctgcgtc	tggctcgagc	caggaccacc	gtggctgctg	tcttctctaa	840
ccggcacctg	gctggagtgt	tcttcaggtc	tgtggtgctg	gccaacctga	ctggcaaaagt	900

gtggatcgcc	tccgaagact	gggccatctc	cacgtacatc	accaatgtgc	ccgggatcca	960
gggcattggg	acgggtgctg	gggtggccat	ccagcagaga	caagtccctg	gcctgaagga	1020
gtttgaagag	tcctatgtcc	aggcagtgat	gggtgctccc	agaacttgcc	cagaggggtc	1080
ctggtgcggc	actaaccagc	tgtgcagggg	gtgtcacgct	ttcacgacat	ggaacatgcc	1140
cgagcttggg	gccttctcca	tgagcgctgc	ctacaatgtg	tatgaggctg	tgtatgctgt	1200
ggccccaggc	ctccaccagc	tcctgggatg	tacctctggg	acctgtgcca	gaggcccagt	1260
ctacccctgg	cagcttcttc	agcagatcta	caagggtgaat	ttccttctac	ataagaagac	1320
tgtagcattc	gatgacaagg	gggaccctct	aggttattat	gacatcatcg	cctgggactg	1380
gaatggacct	gaatggacct	ttgaggtcat	tggttctgcc	tcactgtctc	cagttcatct	1440
agacataaat	aagacaaaaa	tccagtggca	cgggaagaac	aatcagggtg	ctgtgtcagt	1500
gtgtaccagg	gactgtctcg	aagggcacca	caggttggtc	atgggttccc	accactgctg	1560
cttcgagtgc	atgccctgtg	aagctgggac	atttctcaac	acgagtgagc	ttcacacctg	1620
ccagccttgc	ggaacagaag	aatgggcccc	tgaggggagc	tcagcctgct	tctcacgcac	1680
cgtggagttc	ttgggggtgg	atgaacccat	ctctttgggtg	ctattagcag	ctaacacgct	1740
attgctgctg	ctgctgattg	ggactgctgg	cctgtttgcc	tggcgtcttc	acacgcctgt	1800
tgtgaggtca	gctgggggta	ggctgtgctt	cctcatgctg	ggttcccttg	tagctgggag	1860
ttgcagcctc	tacagcttct	tcgggaagcc	cacggtgccc	gcgtgcttgc	tgcgtcagcc	1920
cctcttttct	ctcgggtttg	ccattttcct	ctcctgtctg	acaatccgct	ccttccaaact	1980
ggteatcatc	ttcaagtttt	ctaccaaggt	acccacattc	taccacactt	gggccccaaa	2040
ccatggtgcc	ggaatattcg	tcattgtcag	ctccacggtc	catttggttc	tctgtctcac	2100
gtggcttgca	atgtggaccc	cagggccac	caggagtagc	cagcgcttcc	cccactctgt	2160
gattcttgag	tgcacagagg	tcaactctgt	gggcttctcg	gtggctttcg	cacacaacat	2220
cctcctctcc	atcagcacct	ttgtctgcag	ctacctgggt	aagggaactgc	cggagaacta	2280
taacgaagcc	aaatgtgtca	ccttcagcct	gtcctccac	ttcgtatcct	ggatcgcttt	2340
cttcaccatg	tccagcattt	accagggcag	ctacctacc	gcgggtcaatg	tgctggcagg	2400
gctggccact	ctgagtggcg	gcttcagcgg	ctatttcctc	cctaaatgct	acgtgattct	2460
ctgccgtcca	gaactcaaca	acacagaaca	ctttcaggcc	tccatccagg	actacacgag	2520
gcgctgcggc	actacctgag	gcgctgcggc	actacctgag	gcgctgcggc	actacctga	2579

<210> 6

<211> 2333

<212> DNA

<213> Homo sapiens

<220>

<223> human T1R1 sweet taste receptor

<400> 6

aggctcttgta	gcttcaatga	gcatggctac	cacctcttcc	aggctatgcg	gcttgggggtt	60
gaggagataa	acaactccac	ggccctgctg	cccaacatca	ccctggggta	ccagctgtat	120
gatgtgtgtt	ctgactctgc	caatgtgtat	gccacgctga	gagtgtctct	cctgccaggg	180
caacaccaca	tagagctcca	aggagacctt	ctccactatt	cccctacggg	gctggcagtg	240
attgggcctg	acagcaccaa	ccgtgctgcc	accacagccg	ccctgctgag	ccctttcctg	300
gtgcatatta	gctatgcggc	cagcagcgag	acgctcagcg	tgaagcggca	gtatccctct	360
ttcctgcgca	ccatccccaa	tgacaagtac	caggtggaga	ccatggtgct	gctgctgcag	420
aagttcgggt	ggacctggat	ctctctgggt	ggcagcagtg	acgactatgg	gcagctaggg	480
gtgcaggcac	tggagaacca	ggccctgggt	aggggcacat	gcattgcttt	caaggacatc	540
atgcccttct	ctgcccaggt	ggcgatgag	aggatgcagt	gcctcatgcg	ccacctggcc	600
caggccgggg	ccaccgtcgt	ggttgttttt	tccagccggc	agttggccag	ggtgtttttc	660
gagtcctggt	tgtgaccaa	cctgactggc	aagggtgtgg	tcgcctcaga	agcctggggc	720
ctctccaggc	acatcactgg	ggtgcccggg	atccagcgca	ttgggatggg	gctgggcgtg	780
gccatccaga	agagggtgtg	ccctggcctg	aaggcgtttg	aagaagccta	tgcccggggc	840
gacaaggagg	cccctaggcc	ttgcacaagg	gctcctgggt	cagcagcaat	cagctctgca	900
gagaatgcca	agctttcatg	gcacacacga	tgcccaagct	caaagccttc	tccatgagtt	960
ctgcctacaa	cgcataaccg	gctgtgtatg	cgggtggcca	tggcctccac	cagctcctgg	1020
gctgtgcctc	tgagctctgt	tccaggggcc	gagcttacc	ctggcagctt	ttggagcaga	1080
tccacaagggt	gcatttccct	ctacacaagg	acactgtggc	gtttaatgac	aacagagatc	1140
ccctcagtag	ctataacata	attgcctggg	actggaatgg	acccaagtgg	accttcacgg	1200
tcctcggttc	ctccacatgg	tctccagttc	agctaaacat	aaatgagacc	aaaatccagt	1260
ggcacggaaa	gaaccaccag	gtgcctaagt	ctgtgtgttc	cagcgactgt	cttgaagggc	1320

```

accagcgagt gggttacgggt ttccatcact gctgctttga gtgtgtgccc tgtggggctg 1380
ggaccttcct caacaagagc gagctctaca gatgccagcc ttgtggaaca gaagagtggg 1440
cacctgaggg aagccagacc tgcttcccgc gactgtgggt gtttttggct ttgctgagc 1500
acacctcttg ggtgctgctg gcagctaaca cgctgctgct gctgctgctg cttgggactg 1560
ctggcctgtt tgccctggcac ctagacaccc ctgtgggtgag gtcagcaggg ggccgcctgt 1620
gctttcttat gctgggctcc ctggcagcag gtagtggcag cctctatggc ttctttgggg 1680
aaccacaag gcctgcgtgc ttgctacgcc aggccctctt tgcccttggg ttcaccatct 1740
tcctgtcctg cctgacagtt cgctcattcc aactaatcat catcttcaag ttttccacca 1800
aggtacctac attctaccac gcctgggtcc aaaaccacgg tgctggcctg tttgtgatga 1860
tcagctcagc ggcccagctg cttatctgtc taacttggct ggtggtgtgg accccactgc 1920
ctgctaggga ataccagcgc ttcccccatc tgggtatgct tgagtgcaca gagaccaact 1980
ccctgggctt catactggcc ttctctaca atggcctcct ctccatcagt gcctttgcct 2040
gcagctacct gggtaaggac ttgccagaga actacaacga ggccaaatgt gtcaccttca 2100
gcctgctctt caacttcgtg tcctggatcg ccttcttcac cagggccagc gtctacgacg 2160
gcaagtacct gcctgcggcc aacatgatgg ctgggctgag cagcctgagc agcggcttcg 2220
gtgggtatct tctgcctaag tgctacgtga tcctctgccg cccagacctc aacagcacag 2280
agcacttcca ggcctccatt caggactaca cgaggcgctg cggctccacc tga 2330

```

<210> 7

<211> 843

<212> PRT

<213> Rattus sp.

<220>

<223> rat T1R2 sweet taste receptor

<400> 7

```

Met Gly Pro Gln Ala Arg Thr Leu Cys Leu Leu Ser Leu Leu Leu His
  1              5              10              15

```

```

Val Leu Pro Lys Pro Gly Lys Leu Val Glu Asn Ser Asp Phe His Leu
          20              25              30

```

```

Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
    35              40              45

```

```

Lys Ser Ile Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
    50              55              60

```

```

Phe Thr Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
    65              70              75              80

```

```

Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu
          85              90              95

```

```

Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile His
    100              105              110

```

```

Pro Gly Leu Tyr Phe Leu Ala Gln Asp Asp Asp Leu Leu Pro Ile Leu
    115              120              125

```

```

Lys Asp Tyr Ser Gln Tyr Met Pro His Val Val Ala Val Ile Gly Pro
    130              135              140

```

```

Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser His Phe
    145              150              155              160

```

```

Leu Ile Pro Gln Ile Thr Tyr Ser Ala Ile Ser Asp Lys Leu Arg Asp
    165              170              175

```

Lys Arg His Phe Pro Ser Met Leu Arg Thr Val Pro Ser Ala Thr His  
 180 185 190  
 His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp  
 195 200 205  
 Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His  
 210 215 220  
 Leu Leu Ser Gln Arg Leu Thr Lys Thr Ser Asp Ile Cys Ile Ala Phe  
 225 230 235 240  
 Gln Glu Val Leu Pro Ile Pro Glu Ser Ser Gln Val Met Arg Ser Glu  
 245 250 255  
 Glu Gln Arg Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser  
 260 265 270  
 Ala Arg Val Val Val Val Phe Ser Pro Glu Leu Ser Leu Tyr Ser Phe  
 275 280 285  
 Phe His Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala  
 290 295 300  
 Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu  
 305 310 315 320  
 Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile  
 325 330 335  
 Pro Gly Phe Ser Gln Phe Arg Val Arg Arg Asp Lys Pro Gly Tyr Pro  
 340 345 350  
 Val Pro Asn Thr Thr Asn Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp  
 355 360 365  
 Ala Cys Leu Asn Thr Thr Lys Ser Phe Asn Asn Ile Leu Ile Leu Ser  
 370 375 380  
 Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala  
 385 390 395 400  
 His Ala Leu His Arg Leu Leu Gly Cys Asn Arg Val Arg Cys Thr Lys  
 405 410 415  
 Gln Lys Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn  
 420 425 430  
 Phe Thr Leu Leu Gly Asn Arg Leu Phe Phe Asp Gln Gln Gly Asp Met  
 435 440 445  
 Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Asp Leu Ser Gln Asn  
 450 455 460  
 Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Ser Lys Arg Leu Thr  
 465 470 475 480  
 Tyr Ile Asn Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Val  
 485 490 495

Ser	Met	Cys	Ser	Lys	Ser	Cys	Gln	Pro	Gly	Gln	Met	Lys	Lys	Ser	Val	500	505	510
Gly	Leu	His	Pro	Cys	Cys	Phe	Glu	Cys	Leu	Asp	Cys	Met	Pro	Gly	Thr	515	520	525
Tyr	Leu	Asn	Arg	Ser	Ala	Asp	Glu	Phe	Asn	Cys	Leu	Ser	Cys	Pro	Gly	530	535	540
Ser	Met	Trp	Ser	Tyr	Lys	Asn	Asp	Ile	Thr	Cys	Phe	Gln	Arg	Arg	Pro	545	550	555
Thr	Phe	Leu	Glu	Trp	His	Glu	Val	Pro	Thr	Ile	Val	Val	Ala	Ile	Leu	565	570	575
Ala	Ala	Leu	Gly	Phe	Phe	Ser	Thr	Leu	Ala	Ile	Leu	Phe	Ile	Phe	Trp	580	585	590
Arg	His	Phe	Gln	Thr	Pro	Met	Val	Arg	Ser	Ala	Gly	Gly	Pro	Met	Cys	595	600	605
Phe	Leu	Met	Leu	Val	Pro	Leu	Leu	Leu	Ala	Phe	Gly	Met	Val	Pro	Val	610	615	620
Tyr	Val	Gly	Pro	Pro	Thr	Val	Phe	Ser	Cys	Phe	Cys	Arg	Gln	Ala	Phe	625	630	635
Phe	Thr	Val	Cys	Phe	Ser	Ile	Cys	Leu	Ser	Cys	Ile	Thr	Val	Arg	Ser	645	650	655
Phe	Gln	Ile	Val	Cys	Val	Phe	Lys	Met	Ala	Arg	Arg	Leu	Pro	Ser	Ala	660	665	670
Tyr	Ser	Phe	Trp	Met	Arg	Tyr	His	Gly	Pro	Tyr	Val	Phe	Val	Ala	Phe	675	680	685
Ile	Thr	Ala	Ile	Lys	Val	Ala	Leu	Val	Val	Gly	Asn	Met	Leu	Ala	Thr	690	695	700
Thr	Ile	Asn	Pro	Ile	Gly	Arg	Thr	Asp	Pro	Asp	Asp	Pro	Asn	Ile	Met	705	710	715
Ile	Leu	Ser	Cys	His	Pro	Asn	Tyr	Arg	Asn	Gly	Leu	Leu	Phe	Asn	Thr	725	730	735
Ser	Met	Asp	Leu	Leu	Leu	Ser	Val	Leu	Gly	Phe	Ser	Phe	Ala	Tyr	Met	740	745	750
Gly	Lys	Glu	Leu	Pro	Thr	Asn	Tyr	Asn	Glu	Ala	Lys	Phe	Ile	Thr	Leu	755	760	765
Ser	Met	Thr	Phe	Ser	Phe	Thr	Ser	Ser	Ile	Ser	Leu	Cys	Thr	Phe	Met	770	775	780
Ser	Val	His	Asp	Gly	Val	Leu	Val	Thr	Ile	Met	Asp	Leu	Leu	Val	Thr	785	790	795
Val	Leu	Asn	Phe	Leu	Ala	Ile	Gly	Leu	Gly	Tyr	Phe	Gly	Pro	Lys	Cys	805	810	815

Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn  
820 825 830

Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser  
835 840

<210> 8  
<211> 843  
<212> PRT  
<213> Mus musculus

<220>  
<223> mouse T1R2 sweet taste receptor

<400> 8  
Met Gly Pro Gln Ala Arg Thr Leu His Leu Leu Phe Leu Leu His  
1 5 10 15

Ala Leu Pro Lys Pro Val Met Leu Val Gly Asn Ser Asp Phe His Leu  
20 25 30

Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val  
35 40 45

Lys Ser Val Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu  
50 55 60

Tyr Asn Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe  
65 70 75 80

Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu  
85 90 95

Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile Gln  
100 105 110

Pro Gly Leu Tyr Phe Leu Ser Gln Ile Asp Asp Phe Leu Pro Ile Leu  
115 120 125

Lys Asp Tyr Ser Gln Tyr Arg Pro Gln Val Val Ala Val Ile Gly Pro  
130 135 140

Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser Tyr Phe  
145 150 155 160

Leu Val Pro Gln Val Thr Tyr Ser Ala Ile Thr Asp Lys Leu Gln Asp  
165 170 175

Lys Arg Arg Phe Pro Ala Met Leu Arg Thr Val Pro Ser Ala Thr His  
180 185 190

His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp  
195 200 205

Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His  
210 215 220

Leu Leu Ser Gln Arg Leu Thr Asn Thr Gly Asp Ile Cys Ile Ala Phe  
225 230 235 240

16



Ala	Phe	Leu	Glu	Trp	His	Glu	Val	Pro	Thr	Ile	Val	Val	Thr	Ile	Leu	565	570	575
Ala	Ala	Leu	Gly	Phe	Ile	Ser	Thr	Leu	Ala	Ile	Leu	Leu	Ile	Phe	Trp	580	585	590
Arg	His	Phe	Gln	Thr	Pro	Met	Val	Arg	Ser	Ala	Gly	Gly	Pro	Met	Cys	595	600	605
Phe	Leu	Met	Leu	Val	Pro	Leu	Leu	Leu	Ala	Phe	Gly	Met	Val	Pro	Val	610	615	620
Tyr	Val	Gly	Pro	Pro	Thr	Val	Phe	Ser	Cys	Phe	Cys	Arg	Gln	Ala	Phe	625	630	635
Phe	Thr	Val	Cys	Phe	Ser	Val	Cys	Leu	Ser	Cys	Ile	Thr	Val	Arg	Ser	645	650	655
Phe	Gln	Ile	Val	Cys	Val	Phe	Lys	Met	Ala	Arg	Arg	Leu	Pro	Ser	Ala	660	665	670
Tyr	Gly	Phe	Trp	Met	Arg	Tyr	His	Gly	Pro	Tyr	Val	Phe	Val	Ala	Phe	675	680	685
Ile	Thr	Ala	Val	Lys	Val	Ala	Leu	Val	Ala	Gly	Asn	Met	Leu	Ala	Thr	690	695	700
Thr	Ile	Asn	Pro	Ile	Gly	Arg	Thr	Asp	Pro	Asp	Asp	Pro	Asn	Ile	Ile	705	710	715
Ile	Leu	Ser	Cys	His	Pro	Asn	Tyr	Arg	Asn	Gly	Leu	Leu	Phe	Asn	Thr	725	730	735
Ser	Met	Asp	Leu	Leu	Leu	Ser	Val	Leu	Gly	Phe	Ser	Phe	Ala	Tyr	Val	740	745	750
Gly	Lys	Glu	Leu	Pro	Thr	Asn	Tyr	Asn	Glu	Ala	Lys	Phe	Ile	Thr	Leu	755	760	765
Ser	Met	Thr	Phe	Ser	Phe	Thr	Ser	Ser	Ile	Ser	Leu	Cys	Thr	Phe	Met	770	775	780
Ser	Val	His	Asp	Gly	Val	Leu	Val	Thr	Ile	Met	Asp	Leu	Leu	Val	Thr	785	790	795
Val	Leu	Asn	Phe	Leu	Ala	Ile	Gly	Leu	Gly	Tyr	Phe	Gly	Pro	Lys	Cys	805	810	815
Tyr	Met	Ile	Leu	Phe	Tyr	Pro	Glu	Arg	Asn	Thr	Ser	Ala	Tyr	Phe	Asn	820	825	830
Ser	Met	Ile	Gln	Gly	Tyr	Thr	Met	Arg	Lys	Ser						835	840	

<210> 9

<211> 838

<212> PRT

<213> Homo sapiens

<220>

<223> human T1R2 sweet taste receptor

<400> 9

Met Gly Pro Arg Ala Lys Thr Ile Cys Ser Leu Phe Phe Leu Leu Trp  
1 5 10 15  
Val Leu Ala Glu Pro Ala Glu Asn Ser Asp Phe Tyr Leu Pro Gly Asp  
20 25 30  
Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile  
35 40 45  
Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val  
50 55 60  
Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu  
65 70 75 80  
Glu Ile Asn Asn Asp Ser Ser Leu Leu Pro Gly Val Leu Leu Gly Tyr  
85 90 95  
Glu Ile Val Asp Val Cys Tyr Ile Ser Asn Asn Val Gln Pro Val Leu  
100 105 110  
Tyr Phe Leu Ala His Glu Asp Asn Leu Leu Pro Ile Gln Glu Asp Tyr  
115 120 125  
Ser Asn Tyr Ile Ser Arg Val Val Ala Val Ile Gly Pro Asp Asn Ser  
130 135 140  
Glu Ser Val Met Thr Val Ala Asn Phe Leu Ser Leu Phe Leu Leu Pro  
145 150 155 160  
Gln Ile Thr Tyr Ser Ala Ile Ser Asp Glu Leu Arg Asp Lys Val Arg  
165 170 175  
Phe Pro Ala Leu Leu Arg Thr Thr Pro Ser Ala Asp His His Val Glu  
180 185 190  
Ala Met Val Gln Leu Met Leu His Phe Arg Trp Asn Trp Ile Ile Val  
195 200 205  
Leu Val Ser Ser Asp Thr Tyr Gly Arg Asp Asn Gly Gln Leu Leu Gly  
210 215 220  
Glu Arg Val Ala Arg Arg Asp Ile Cys Ile Ala Phe Gln Glu Thr Leu  
225 230 235 240  
Pro Thr Leu Gln Pro Asn Gln Asn Met Thr Ser Glu Glu Arg Gln Arg  
245 250 255  
Leu Val Thr Ile Val Asp Lys Leu Gln Gln Ser Thr Ala Arg Val Val  
260 265 270  
Val Val Phe Ser Pro Asp Leu Thr Leu Tyr His Phe Phe Asn Glu Val  
275 280 285  
Leu Arg Gln Asn Phe Thr Gly Ala Val Trp Ile Ala Ser Glu Ser Trp  
290 295 300

Ala	Ile	Asp	Pro	Val	Leu	His	Asn	Leu	Thr	Glu	Leu	Gly	His	Leu	Gly	305	310	315	320
Thr	Phe	Leu	Gly	Ile	Thr	Ile	Gln	Ser	Val	Pro	Ile	Pro	Gly	Phe	Ser	325	330	335	
Glu	Phe	Arg	Glu	Trp	Gly	Pro	Gln	Ala	Gly	Pro	Pro	Pro	Leu	Ser	Arg	340	345	350	
Thr	Ser	Gln	Ser	Tyr	Thr	Cys	Asn	Gln	Glu	Cys	Asp	Asn	Cys	Leu	Asn	355	360	365	
Ala	Thr	Leu	Ser	Phe	Asn	Thr	Ile	Leu	Arg	Leu	Ser	Gly	Glu	Arg	Val	370	375	380	
Val	Tyr	Ser	Val	Tyr	Ser	Ala	Val	Tyr	Ala	Val	Ala	His	Ala	Leu	His	385	390	395	400
Ser	Leu	Leu	Gly	Cys	Asp	Lys	Ser	Thr	Cys	Thr	Lys	Arg	Val	Val	Tyr	405	410	415	
Pro	Trp	Gln	Leu	Leu	Glu	Glu	Ile	Trp	Lys	Val	Asn	Phe	Thr	Leu	Leu	420	425	430	
Asp	His	Gln	Ile	Phe	Phe	Asp	Pro	Gln	Gly	Asp	Val	Ala	Leu	His	Leu	435	440	445	
Glu	Ile	Val	Gln	Trp	Gln	Trp	Asp	Arg	Ser	Gln	Asn	Pro	Phe	Gln	Ser	450	455	460	
Val	Ala	Ser	Tyr	Tyr	Pro	Leu	Gln	Arg	Gln	Leu	Lys	Asn	Ile	Gln	Asp	465	470	475	480
Ile	Ser	Trp	His	Thr	Val	Asn	Asn	Thr	Ile	Pro	Met	Ser	Met	Cys	Ser	485	490	495	
Lys	Arg	Cys	Gln	Ser	Gly	Gln	Lys	Lys	Lys	Pro	Val	Gly	Ile	His	Val	500	505	510	
Cys	Cys	Phe	Glu	Cys	Ile	Asp	Cys	Leu	Pro	Gly	Thr	Phe	Leu	Asn	His	515	520	525	
Thr	Glu	Asp	Glu	Tyr	Glu	Cys	Gln	Ala	Cys	Pro	Asn	Asn	Glu	Trp	Ser	530	535	540	
Tyr	Gln	Ser	Glu	Thr	Ser	Cys	Phe	Lys	Arg	Gln	Leu	Val	Phe	Leu	Glu	545	550	555	560
Trp	His	Glu	Ala	Pro	Thr	Ile	Ala	Val	Ala	Leu	Leu	Ala	Ala	Leu	Gly	565	570	575	
Phe	Leu	Ser	Thr	Leu	Ala	Ile	Leu	Val	Ile	Phe	Trp	Arg	His	Phe	Gln	580	585	590	
Thr	Pro	Ile	Val	Arg	Ser	Ala	Gly	Gly	Pro	Met	Cys	Phe	Leu	Met	Leu	595	600	605	
Thr	Leu	Leu	Leu	Val	Ala	Tyr	Met	Val	Val	Pro	Val	Tyr	Val	Gly	Pro	610	615	620	

Pro Lys Val Ser Thr Cys Leu Cys Arg Gln Ala Leu Phe Pro Leu Cys  
 625 630 635 640  
 Phe Thr Ile Cys Ile Ser Cys Ile Ala Val Arg Ser Phe Gln Ile Val  
 645 650 655  
 Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp  
 660 665 670  
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu  
 675 680 685  
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Arg Pro Gln Ser His  
 690 695 700  
 Pro Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys Asn  
 705 710 715 720  
 Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu Leu  
 725 730 735  
 Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu Pro  
 740 745 750  
 Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe Tyr  
 755 760 765  
 Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser Gly  
 770 775 780  
 Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu Leu  
 785 790 795 800  
 Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu Phe  
 805 810 815  
 Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln Gly  
 820 825 830  
 Tyr Thr Met Arg Arg Asp  
 835

<210> 10  
 <211> 2993  
 <212> DNA  
 <213> Rattus sp.

<220>  
 <223> rat T1R2 sweet taste receptor

<400> 10  
 cactttgctg tcatgggtcc ccaggcaagg acactctgct tgctgtctct cctgctgcat 60  
 gttctgccta agccaggcaa gctggtagag aactctgact tccacctggc cggggactac 120  
 ctctgggtg gcctctttac cctccatgcc aacgtgaaga gcatctccca cctcagctac 180  
 ctgcaggtgc ccaagtgc aa tgagttcacc atgaagggtg tgggctacaa cctcatgcag 240  
 gccatgcgtt tcgctgtgga ggagatcaac aactgtagct cctgctacc cggcgtgctg 300  
 ctcggtacg agatgggtgga tgtctgttac ctctccaaca atatccaccc tgggctctac 360  
 ttctggcac aggacgacga cctcctgccc atcctcaaag actacagcca gtacatgccc 420  
 cacgtggtgg ctgtcattgg ccccgacaac tctgagtcog ccattaccgt gtccaacatt 480  
 ctctctcatt tcctcatccc acagatcaca tacagcgcca tctccgacaa gctgcgggac 540

aagcggcact	tccctagcat	gctacgcaca	gtgcccagcg	ccaccaccca	catcgaggcc	600
atggtgcagc	tgatggttca	cttccaatgg	aactggattg	tggtgctggt	gagcgacgac	660
gattacggcc	gcgagaacag	ccacctgttg	agccagcgtc	tgaccaaaac	gagcgacatc	720
tgcatgtcct	tccaggaggt	tctgcccata	cctgagtgca	gccagggtcat	gagggtccgag	780
gagcagagac	aactggacaa	catcctggac	aagctgcggc	ggacctcggc	gcgcgtcgtg	840
gtggtgttct	cgcccagagct	gagcctgtat	agcttctttc	acgagggtgct	ccgctggaac	900
ttcacgggtt	ttgtgtggat	cgctctgtag	tcctgggcta	tcgaccaggt	tctgcataac	960
ctcacggagc	tgcgccacac	gggtactttt	ctgggcgtca	ccatccagag	ggtgtccatc	1020
cctggcttca	gtcagttccg	agtgcgccgt	gacaagccag	ggtatcccgt	gcctaacacg	1080
accaacctgc	ggacgacctg	caaccaggac	tgtgacgcct	gcttgaacac	caccaagtcc	1140
ttcaacaaca	tccttatact	ttcgggggag	cgcgtggtct	acagcgtgta	ctcggcagtt	1200
tacgcgggtg	cccatgccct	ccacagactc	ctcggtgta	accgggtccg	ctgcaccaag	1260
caaaaggctc	accgtggca	gctactcagg	gagatctggc	acgtcaactt	cacgctcctg	1320
ggtaaccggc	tcttctttga	ccaacaaggg	gacatgccga	tgctcttgga	catcatccag	1380
tggcagtggg	acctgagcca	gaatcccttc	caaagcatcg	cctcctattc	tcccaccagc	1440
aagaggctaa	cctacattaa	caatgtgtcc	tggtacaccc	ccaacaacac	ggtccctgtc	1500
tccatgtgtt	ccaagagctg	ccagccaggg	caaataaaaa	agtctgtggg	cctccaccct	1560
tggtgtctcg	agtgtctgga	ttgtatgccg	ggcacctacc	tcaaccgctc	agcagatgag	1620
tttaactgtc	tgctctgccc	gggttccatg	tggtcctaca	agaacgacat	cacttgcttc	1680
cagcggcgcc	ctaccttctt	ggagtggcac	gaagtgccta	ccatcgtggt	ggccatactg	1740
gctgcccctg	gcttcttcag	tacactggcc	attcttttca	tcttctggag	acatttccag	1800
acacccatgg	tgcgctcgcc	cggtgggccc	atgtgtctcc	tgatgtctcg	gcccctgctg	1860
ctggcgcttg	ggatgggtgcc	cgtgtatgtg	gggcccccca	cgggtctctc	atgtctctgc	1920
cgacaggctt	tcttcaccgt	ctgtcttctc	atctgcctat	cctgcatac	cgtgcgtctc	1980
ttccagatcg	tgtgtgtctt	caagatggcc	agacgcctgc	caagtgccta	cagtttttgg	2040
atgcgttacc	acggggcccta	tgtcttcgtg	gccttcatca	cggccatcaa	ggtggccctg	2100
gtggtgggca	acatgctggc	caccaccatc	aaccccatg	gcccggaccga	cccggatgac	2160
cccaacatca	tgatcctctc	gtgccaccct	aactaccgca	acgggctact	gttcaacacc	2220
agcatggact	tgctgctgtc	tgtgctgggt	ttcagcttcg	cttacatggg	caaggagctg	2280
cccaccaact	acaacgaagc	caagttcatc	actctcagca	tgaccttctc	cttcacctcc	2340
tccatctccc	tctgcacctt	catgtctgtg	cacgacggcg	tgctgggtcac	catcatggac	2400
ctcctgggtca	ctgtgctcaa	cttcctggcc	atcggttggg	gatacttttg	ccccaaagtg	2460
tacatgatcc	ttttctaccc	ggagcgcaac	acctcagcct	atttcaatag	catgatccag	2520
ggctacacca	tgaggaagag	ctagctccgc	ccaccggcct	cagcagcaga	gcccccgcc	2580
acgttaaatg	tgttcctctg	ccattctctg	cagcgtagct	atttttacc	acatagcgct	2640
taaaataccc	atgatgcact	ctccccgcac	ccccaaagca	tttcaactgg	caggacctac	2700
caccacttta	tagatgaaac	caccaaggcg	ccctatgggg	ctccaaggat	ggcctaccac	2760
tgccatctgg	tggtcacagt	gagcacatgc	gggcctgtgg	ccatggctcc	cagccagctg	2820
gtggctagtg	gctgtgaggc	cagatgtctg	ttgtatctgag	ttcctgggaa	gcagagactg	2880
gggctcctgt	gttctaattg	tcagatgggc	atcatggggc	cttcattatt	gcttacgaat	2940
aaacttcctt	ccggtgaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaa	2993

<210> 11

<211> 2532

<212> DNA

<213> Mus musculus

<220>

<223> mouse T1R2 sweet taste receptor

<400> 11

atgggacccc	aggcgaggac	actccatttg	ctgtttctcc	tgctgcatgc	tctgcctaag	60
ccagtcacgc	tggtagggaa	ctccgacttt	cacctggctg	gggactacct	cctgggtggc	120
ctcttttacc	tccatgccaa	cgtgaagagt	gtctctcacc	tcagctacct	gcaggtgcc	180
aagtgcaatg	agtacaacat	gaaggtgttg	ggctacaacc	tcatgcaggc	catgcgattc	240
gccgtggagg	aaatcaacaa	ctgtagctct	tgctgccc	gcgtgctgct	cggctacgag	300
atgggtggatg	tctgctacct	ctccaacaat	atccagcctg	ggctctactt	cctgtcacag	360
atagatgact	tcctgcccac	cctcaaagac	tacagccagt	acaggcccca	agtggtggct	420
gttattggcc	cagacaactc	tgagtctgcc	atcaccgtgt	ccaacattct	ctcctacttc	480
ctcgtgccac	agggtcacata	tagcgccatc	accgacaagc	tgcaagacaa	gcggcgcttc	540

cctgccatgc	tgcgcactgt	gcccagcgcc	accaccaca	tgcaggccat	ggtgcaactg	600
atggttca	tccagtggaa	ctggatcgtg	gtgctgggtga	gcgatgacga	ttatggccga	660
gagaacagcc	acctgctgag	ccagcgtctg	accaacactg	gcgacatctg	cattgccttc	720
caggagggttc	tgcccgtacc	agaacccaac	caggctgtga	ggcctgagga	gcaggaccaa	780
ctggacaaca	tcctggacaa	gctgcggcgg	acttcggcgc	gtgtgggtgg	gatattctcg	840
ccggagctga	gcctgcacaa	cttcttccgt	gaggtgctgc	gctggaactt	cacgggcttt	900
gtgtggattg	cctctgagtc	ctgggccatc	gaccctgttc	tacacaacct	cacagagctg	960
cgccacacgg	gcactttcct	gggtgtcacc	atccagaggg	tgtccatccc	tggcttcagc	1020
cagttccgag	tgcgccatga	caagccaggg	tatcgcctgc	ctaaccgagac	cagcctgcgg	1080
actacctgta	accaggactg	cgacgcctgc	atgaacatca	ctgagtcctt	caacaacgtt	1140
ctcatgcttt	cgggggagcg	tgtgggtctac	agcgtgtact	cgcccgctta	cgcggtggcc	1200
cacacctcc	acagactcct	ccactgcaat	caggtccgct	gcaccaagca	aatcgtctat	1260
ccatggcagc	tactcagggg	gatctggcat	gtcaacttca	cgctcctggg	caaccagctc	1320
ttcttcgacg	aacaagggga	catgccgatg	ctcctggaca	tcattccagt	gcagtggggc	1380
ctgagccaga	accccttcca	aagcatcgcc	tcctactccc	ccaccgagac	gaggctgacc	1440
tacattagca	atgtgtcctg	gtacaccccc	aacaacacgg	tcacccatct	catgtgttct	1500
aagagttgcc	agcctgggca	aatgaaaaaa	cccataggcc	tcacccatct	ctgcttcgag	1560
tgtgtggact	gtccgcggga	cacctacctc	aaccgatcag	tagatgagtt	taactgtctg	1620
tcctgcccgg	gttccatgtg	gtcttacaag	aacaacatcg	cttgcttcaa	gcggcggtg	1680
gccttctctg	agtggcacga	agtgcccat	atcgtgggtga	ccatcctggc	cgccctgggc	1740
ttcatcagta	cgctggccat	tctgtctatc	ttctggagac	atttccagac	gcccattggtg	1800
cgctcggcgg	gcggccccc	gtgcttccct	atgctgggtgc	ccctgctgct	ggcggttcggg	1860
atggtccccg	tgtatgtggg	cccccccacg	gtcttctcct	gtttctgccg	ccaggctttc	1920
ttcaccgttt	gcttctccgt	ctgcctctcc	tgcctcacgg	tgcgctcctt	ccagattgtg	1980
tgcgtcttca	agatggccag	acgcctgcc	agcgcctacg	gtttctggat	gcgttaccac	2040
gggcccctacg	tcctcgtggc	cttcctcacg	gccgtcaagg	tggccctggg	ggcgggcaac	2100
atgctggcca	ccaccatcaa	ccccattggc	cggaccgacc	ccgatgaccc	caatatcata	2160
atcctctcct	gccaccctaa	ctaccgcaac	gggctactct	tcaacaccag	catggacttg	2220
ctgctgtccg	tgctgggttt	cagcttcgcg	tacgtgggca	aggaactgcc	caccaactac	2280
aacgaagcca	agttcatcac	cctcagcatg	accttctcct	tcacctcttc	catctccttc	2340
tgcacgttca	tgtctgtcca	cgatggcgtg	ctgggtcacca	tcattggatct	cctgggtcact	2400
gtgctcaact	ttctggccat	cggcttgggg	tactttggcc	ccaaatgtta	catgatecct	2460
ttctaccggg	agcgcaacac	ttcagcttat	ttcaatagca	tgattcaggg	ctacacgatg	2520
aggaagagct	ag					2532

<210> 12

<211> 2010

<212> DNA

<213> Homo sapiens

<220>

<223> human T1R2 sweet taste receptor

<400> 12

atcacctaca	gcgccatcag	cgatgagctg	cgagacaagg	tgcgcttccc	ggctttgctg	60
cgtaccacac	ccagcgccga	ccaccacgtc	gaggccatgg	tgcagctgat	gctgcacttc	120
cgctggaact	ggatcattgt	gctggtgagc	agcgacacct	atggccgcga	caatggccag	180
ctgcttggcg	agcgcggtgg	ccggcgcgac	atctgcatcg	ccttccagga	gacgctgccc	240
acactgcagc	ccaaccagaa	catgacgtca	gaggagcgcc	agcgccctgg	gaccattgtg	300
gacaagctgc	agcagagcac	agcgcgctgc	gtggctcgtg	tctcgcccca	cctgaccctg	360
taccacttct	tcaatgaggt	gctgcgccag	aacttcacgg	gcgcctgtgt	gatgcctctc	420
gagtcctggg	ccatcgaccc	ggtcctgcac	aacctcacgg	agctgggcca	cttgggcacc	480
ttcctgggca	tcaccatcca	gagcgtgccc	atcccgggct	tcagtgaagt	ccgcgagtgg	540
ggcccacagg	ctgggcccgc	accctcagc	aggaccagcc	agagctatac	ctgcaaccag	600
gagtgcgaca	actgcctgaa	cgccaccttg	tccttcaaca	ccattctcag	gctctctggg	660
gagcgtgtcg	tctacagcgt	gtactctgcg	gtctatgctg	tggcccatgc	cctgcacagc	720
ctcctcggct	gtgacaaaag	cacctgcacc	aagagggtgg	tctacccttg	gcagctgctt	780
gaggagatct	ggaaggtcaa	cttcactctc	ctggaccacc	aaatcttctt	cgacccgcaa	840
ggggacgtgg	ctctgcactt	ggagattgtc	cagtggcaat	gggaccggag	ccagaatccc	900
ttccagagcg	tgcctccta	ctaccccctg	cagcgacagc	tgaagaacat	caagacatct	960

ctgcacacccg	tcaacaacac	gatccctatg	tccatgtgtt	ccaagagggtg	ccagtcaggg	1020
caaaagaaga	agcctgtggg	catccacgtc	tgctgcttcg	agtgcacga	ctgccttccc	1080
ggcaccttcc	tcaaccacac	tgaatgcccg	aataacgagt	ggtcctacca	gagtgcagacc	1140
tcctgcttca	agcggcagct	ggtcttcctg	gaatggcatg	aggcaccac	catcgctgtg	1200
gccctgctgg	ccgccctggg	cttcctcagc	accctggcca	tcctggatgat	attctggagg	1260
cacttccaga	caccatagct	tcgctcggct	gggggcccc	tgtgcttcct	gatgctgaca	1320
ctgctgctgg	tggcatacat	ggtgggtccc	gtgtacgtgg	ggccgcccga	ggtctccacc	1380
tgcctctgcc	gccaggccct	ctttcccctc	tgttcacaa	tttgcacatc	ctgtatcgcc	1440
gtgcgttctt	tccagatcgt	ctgcgccttc	aagatggcca	gcccgttccc	acgcgcctac	1500
agctactggg	tccgctacca	ggggccctac	gtctctatgg	catttatcac	ggtactcaaa	1560
atggctcattg	tggtaattgg	catgctggca	cggcctcagt	ccccccccg	tactgacccc	1620
gatgacccca	agatcacaa	tgtctcctgt	aaccccaact	accgcaacag	cctgctgttc	1680
aacaccagcc	tggacctgct	gctctcagtg	gtgggtttca	gcttcgccta	catgggcaaa	1740
gagctgcccc	ccaactacaa	cgaggccaag	ttcatcacc	tcagcatgac	cttctatttc	1800
acctcatccg	tctccctctg	caccttcagt	tctgcctaca	gcgggggtgct	ggtcaccatc	1860
gtggacctct	tggctactgt	gctcaacctc	ctggccatca	gcctgggcta	cttcggcccc	1920
aagtgtctaca	tgatcctctt	ctaccgggag	cgcaacacgc	ccgcctactt	caacagcatg	1980
atccagggct	acaccatgag	gagggactag				2010

<210> 13  
 <211> 3200  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human T1R3 sweet taste receptor genomic

<400> 13						
gctcactcca	tgtgaggccc	cagtcggggc	agccacctgc	cgtgcctggt	ggaagttgcc	60
tctgccatgc	tgggccctgc	tgtcctgggc	ctcagcctct	gggctctcct	gcaccctggg	120
acggggggccc	catttgtgct	gtcacagcaa	cttaggatga	agggggacta	cgtgctgggg	180
gggctgttcc	ccctgggcga	ggccgaggag	gctggcctcc	gcagccggac	acggcccagc	240
agccctgtgt	gcaccaggta	cagagggtgg	acggcctggg	tcggggtcag	ggtgaccagg	300
tctgggggtg	tcctgagctg	gggcccagggt	ggccatctgc	ggttctgtgt	ggccccaggt	360
tctcctcaaa	cgccctgctc	tgggactggt	ccatgaaaat	ggccgtggag	gagatcaaca	420
acaagtccga	tctgctgccc	gggctgcgcc	tgggctacga	cctctttgat	acgtgctcgg	480
agcctgtggt	ggccatgaag	cccagcctca	tgttcttggc	caaggcaggc	agccgcgaca	540
tcgcgcctca	ctgcaactac	acgcagtacc	agccccgtgt	gctggctgtc	atcgggcccc	600
actcgctcaga	gctcgccatg	gtcaccggca	agttcttcag	cttcttcctc	atgccccagg	660
tggcgccccc	caccatcacc	cacccccacc	cagccctgcc	cgtgggagcc	cctgtgtcag	720
gagatgcctc	ttggcccttg	caggtcagct	acggtgctag	catggagctg	ctgagcgccc	780
gggagacctt	cccctccttc	ttccgcaccg	tgccagcgca	ccgtgtgcag	ctgacggccg	840
ccgcggagct	gctgcaggag	ttcggctgga	actgggtggc	cgccctgggc	agcgacgacg	900
agtacggccg	gcagggcctg	agcatcttct	cgccctgggc	cgcggcacgc	ggcatctgca	960
tcgcgcacga	gggctgggtg	ccgctgcccc	gtgccgatga	ctcgcggtcg	gggaaggtgc	1020
aggacgtcct	gcaccagggt	aaccagagca	gcgtgcagggt	ggtgctgctg	ttcgccctccg	1080
tgcacgcccgc	ccacgccttc	ttcaactaca	gcatacagcag	caggctctcg	cccaagggtgt	1140
gggtggccag	cgaggcctgg	ctgacctctg	acctggtcat	ggggctgccc	ggcatggccc	1200
agatgggcac	ggtgcttggc	ttcctccaga	ggggtgccca	gctgcacgag	ttccccagct	1260
acgtgaagac	gcacctggcc	ctggccaccg	acccggcctt	ctgctctgcc	ctgggcgaga	1320
gggagcaggg	tctggaggag	gacgtggtgg	gccagcgctg	cccgcagtggt	gactgcatca	1380
cgctgcagaa	cgtgagcgca	gggctaaatc	accaccagac	gttctctgtc	tacgcagctg	1440
tgtatagcgt	ggcccaggcc	ctgcacaaca	ctcttcagtg	caacgcctca	ggctgccccg	1500
cgcaggaccc	cgtgaagccc	tggcagggtga	gcccgggaga	tgggggtgtg	ctgtcctctg	1560
catgtgcccc	ggccaccagg	cacggccacc	acgcctgagc	tggagggtggc	tggcggtcca	1620
gccccgtccc	ccgcccgcag	ctcctggaga	acatgtacaa	cctgaccttc	cacgtgggcg	1680
ggctgcccgt	gcggttcgac	agcagcgga	acgtggacat	ggagtacgac	ctgaagctgt	1740
gggtgtggca	gggctcagtg	cccaggctcc	acgacgtggg	caggttcaac	ggcagcctca	1800
ggacagagcg	cctgaagatc	cgctggcaca	cgtctgacaa	ccagggtgag	tgagggtggg	1860
tgtgccaggc	gtgcccgtgg	tagccccgcg	ggcaggggcg	agcctggggg	tgggggcccgt	1920

tccagtctcc	cgtgggcatg	cccagccgag	cagagccaga	ccccaggcct	gtgcgcagaa	1980
gcccgtgtcc	cggtgctcgc	ggcagtgcc	ggagggccag	gtgcgcggg	tcaaggggtt	2040
ccactcctgc	tgctacgact	gtgtggactg	cgaggcgggc	agctaccggc	aaaacccagg	2100
tgagccgect	tcccggcagg	cgggggtggg	aacgcagcag	gggaggggtcc	tgccaagtcc	2160
tgactctgag	accagagccc	acaggggtaca	agacgaacac	ccagcgcctt	tctcctctct	2220
cacagacgac	atcgcttgca	ccttttgtgg	ccaggatgag	tgggtcccgg	agcgaagcac	2280
acgctgtctc	cgccgcaggt	ctcggttctt	ggcatggggc	gagccggctg	tgctgctgct	2340
gctcctgctg	ctgagcctgg	cgctgggcct	tgtgctggct	gctttggggc	tggtcgttca	2400
ccatcggggac	agcccactgg	ttcaggcctc	ggggggggccc	ctggcctgct	ttggcctggt	2460
gtgcctgggc	ctgggtctgcc	tcagcgtcct	cctgttccct	ggccagccca	gccctgcccg	2520
atgcctggcc	cagcagccct	tgteccacct	cccgtcacg	ggctgcctga	gcacactctt	2580
cctgcaggcg	gcccagatct	tcgtggagtc	gtaactgcct	ctgagctggg	cagaccggct	2640
gagtggctgc	ctgcgggggc	cctgggcctg	gctgggtggg	ctgctggcca	tgctgggtga	2700
ggctgcactg	tgacactggg	acctgggtgg	cttcccgcgc	gaggtgggtga	cggactggca	2760
catgctgccc	acggaggcgc	tggtgcactg	ccgcacacgc	tcctgggtca	gcttcggcct	2820
agcgcacgcc	accaatgcca	cgctggcctt	tctctgtctt	ctgggcactt	tcctgggtgcg	2880
gagccagccg	ggctgctaca	accgtgcccg	tggcctcacc	tttgccatgc	tggcctactt	2940
catcacctgg	gtctcctttg	tgcccctcct	ggccaatgtg	caggtgggtcc	tcaggcccgc	3000
cgtgcagatg	ggcgccctcc	tgctctgtgt	cctgggcata	ctggctgcct	tccacctgcc	3060
caggtgttac	ctgctcatgc	ggcagccagg	gctcaacacc	cccagattct	tcctgggagg	3120
gggccttggg	gatgcccaag	gccagaatga	cgggaacaca	ggaaatcagg	ggaaacatga	3180
gtgacccaac	cctgtgatct					3200

<210> 14

<211> 2559

<212> DNA

<213> Homo sapiens

<220>

<223> human T1R3 sweet taste receptor CDS

<400> 14

atgctggggc	ctgctgtcct	gggcctcagc	ctctgggctc	tcctgcaccc	tgggacgggg	60
gccccattgt	gcctgtcaca	gcaacttagg	atgaaggggg	actacgtgct	gggggggctg	120
ttccccctgg	gcgaggccga	ggaggtggc	ctccgcagcc	ggacacggcc	cagcagccct	180
gtgtgcacca	ggttctcctc	aaacggcctg	ctctgggcac	tggccatgaa	aatggccgtg	240
gaggagatca	acaacaagtc	ggatctgctg	cccgggctgc	gcctgggcta	cgacctcttt	300
gatactgtgt	cggagcctgt	ggtggccatg	aagcccagcc	tcattgttct	ggccaaggca	360
ggcagccgcg	acatcgccgc	ctactgcaac	tacacgcagt	accagccccg	tgtgctggct	420
gtcatcgggc	cccactcgtc	agagctcgcc	atggtcaccc	gcaagtctct	cagcttcttc	480
ctcatgcccc	aggtcagcta	cggtgctagc	atggagctgc	tgagcgcccc	ggagaccttc	540
ccctccttct	tcgcaccctg	gcccagcgac	cgtgtgcagc	tgacggccgc	cgcggagctg	600
ctgcaggagt	tcggctggaa	ctgggtggcc	gccctgggca	gcgacgacga	gtacggccgg	660
cagggcctga	gcatcttctc	ggccctggcc	gcggcacgcg	gcatctgcat	cgcgcacgag	720
ggcctgggtg	cgctgccccg	tgccgatgac	tcgcggctgg	ggaaggtgca	ggacgtcctg	780
caccaggtga	accagagcag	cgtgcagggt	gtgctgctgt	tcgcctccgt	gcacgcgcgc	840
cacgcccctc	tcaactacag	catcagcagc	aggctctcgc	ccaaggtgtg	ggtggccagc	900
gaggcctggc	tgacctctga	cctggtcatt	gggctgcccc	gcatggccca	gatgggcacg	960
gtgcttggct	tcctccagag	gggtgcccag	ctgcacagat	tcctccagta	cgtgaagacg	1020
cacctggccc	tggccaccga	cccggccttc	tgctctgccc	tgggcgagag	ggagcagggt	1080
ctggaggagg	acgtgggtgg	ccagcgtgct	ccgcagtggt	actgcatcac	gctgcagaac	1140
gtgagcgcag	ggctaaatca	ccaccagacg	ttctctgtct	acgcagctgt	gtatagcgtg	1200
gcccaggccc	tgcaacaacac	tcttcagtgc	aacgcctcag	gctgccccgc	gcaggacccc	1260
gtgaagccct	ggcagctcct	ggagaacatg	tacaacctga	ccttccacgt	gggcgggctg	1320
ccgctgcggg	tcgacagcag	cggaaacgtg	gacatggagt	acgacctgaa	gctgtgggtg	1380
tggcaggggt	cagtggcccag	gctccacgac	gtgggcagg	tcaacggcag	cctcaggaca	1440
gagcgcctga	agatccgctg	gcacacgtct	gacaaccaga	agcccgtgtc	ccggtgctcg	1500
cggcagtgcc	aggaggggcca	ggtgcgcggg	gtcaaggggt	tcactcctg	ctgctacgac	1560
tgtgtggact	gcgaggcggg	cagctaccgg	caaaacccag	acgacatcgc	ctgcaccttt	1620
tgtggccagg	atgagtggct	cccggagcga	agcacacgct	gcttccgccc	caggtctcgg	1680



```

ttcctggcat ggggcgagcc ggctgtgctg ctgctgctcc tgctgctgag cctggcgctg 1740
ggccttggtg tggctgcttt ggggctgttc gttcaccatc gggacagccc actgggttcag 1800
gcctcggggg gggccctggc ctgctttggc ctgggtgtgc tgggcctggt ctgcctcagc 1860
gtcctcctgt tccctggcca gccagccct gccgatgcc tggcccagca gcccttgctc 1920
cacctccgcg tcacgggctg cctgagcaca ctcttcctgc aggcggccga gatcttcgtg 1980
gagtcagaac tgctctgag ctgggcagac cggctgagtg gctgcctgcg ggggccctgg 2040
gcctggctgg tgggtgctgct ggccatgctg gtggaggtcg cactgtgcac ctggtacctg 2100
gtggccttcc cgccggaggt ggtgacggac tggcacatgc tgcccacgga ggcgctgggtg 2160
cactgcccga cacgctcctg ggtagcttc ggcctagcgc acgccaccaa tgccacgctg 2220
gcctttctct gcttcctggg cactttcctg gtgcggagcc agccgggctg ctacaaccgt 2280
gcccgtggcc tcacctttgc catgctggcc tacttcatca cctgggtctc ctttgtgccc 2340
ctcctggcca atgtgcaggt ggtcctcagg cccgccgtgc agatgggcgc cctcctgctc 2400
tgtgtcctgg gcatcctggc tgcctccac ctgccaggt gttacctgct catgcggcag 2460
ccagggctca acacccccga gttcttcctg ggagggggcc ctggggatgc ccaaggccag 2520
aatgacggga acacaggaaa tcaggggaaa catgagtga 2559

```

<210> 15

<211> 852

<212> PRT

<213> Homo sapiens

<220>

<223> human T1R3 sweet taste receptor

<400> 15

```

Met Leu Gly Pro Ala Val Leu Gly Leu Ser Leu Trp Ala Leu Leu His
  1              5              10              15

Pro Gly Thr Gly Ala Pro Leu Cys Leu Ser Gln Gln Leu Arg Met Lys
      20              25              30

Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
      35              40              45

Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
      50              55              60

Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
      65              70              75              80

Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
      85              90              95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
      100             105             110

Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
      115             120             125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
      130             135             140

His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe
      145             150             155             160

Leu Met Pro Gln Val Ser Tyr Gly Ala Ser Met Glu Leu Leu Ser Ala
      165             170             175

Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
      180             185             190

```

Gln	Leu	Thr	Ala	Ala	Ala	Glu	Leu	Leu	Gln	Glu	Phe	Gly	Trp	Asn	Trp	195	200	205
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Glu	Tyr	Gly	Arg	Gln	Gly	Leu	Ser	210	215	220
Ile	Phe	Ser	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu	225	230	235
Gly	Leu	Val	Pro	Leu	Pro	Arg	Ala	Asp	Asp	Ser	Arg	Leu	Gly	Lys	Val	245	250	255
Gln	Asp	Val	Leu	His	Gln	Val	Asn	Gln	Ser	Ser	Val	Gln	Val	Val	Leu	260	265	270
Leu	Phe	Ala	Ser	Val	His	Ala	Ala	His	Ala	Leu	Phe	Asn	Tyr	Ser	Ile	275	280	285
Ser	Ser	Arg	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ala	Trp	Leu	290	295	300
Thr	Ser	Asp	Leu	Val	Met	Gly	Leu	Pro	Gly	Met	Ala	Gln	Met	Gly	Thr	305	310	315
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Gln	Leu	His	Glu	Phe	Pro	Gln	325	330	335
Tyr	Val	Lys	Thr	His	Leu	Ala	Leu	Ala	Thr	Asp	Pro	Ala	Phe	Cys	Ser	340	345	350
Ala	Leu	Gly	Glu	Arg	Glu	Gln	Gly	Leu	Glu	Glu	Asp	Val	Val	Gly	Gln	355	360	365
Arg	Cys	Pro	Gln	Cys	Asp	Cys	Ile	Thr	Leu	Gln	Asn	Val	Ser	Ala	Gly	370	375	380
Leu	Asn	His	His	Gln	Thr	Phe	Ser	Val	Tyr	Ala	Ala	Val	Tyr	Ser	Val	385	390	395
Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln	Cys	Asn	Ala	Ser	Gly	Cys	Pro	405	410	415
Ala	Gln	Asp	Pro	Val	Lys	Pro	Trp	Gln	Leu	Leu	Glu	Asn	Met	Tyr	Asn	420	425	430
Leu	Thr	Phe	His	Val	Gly	Gly	Leu	Pro	Leu	Arg	Phe	Asp	Ser	Ser	Gly	435	440	445
Asn	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys	Leu	Trp	Val	Trp	Gln	Gly	Ser	450	455	460
Val	Pro	Arg	Leu	His	Asp	Val	Gly	Arg	Phe	Asn	Gly	Ser	Leu	Arg	Thr	465	470	475
Glu	Arg	Leu	Lys	Ile	Arg	Trp	His	Thr	Ser	Asp	Asn	Gln	Lys	Pro	Val	485	490	495
Ser	Arg	Cys	Ser	Arg	Gln	Cys	Gln	Glu	Gly	Gln	Val	Arg	Arg	Val	Lys	500	505	510

Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	Cys	Glu	Ala	Gly	Ser		
		515					520					525					
Tyr	Arg	Gln	Asn	Pro	Asp	Asp	Ile	Ala	Cys	Thr	Phe	Cys	Gly	Gln	Asp		
	530					535					540						
Glu	Trp	Ser	Pro	Glu	Arg	Ser	Thr	Arg	Cys	Phe	Arg	Arg	Arg	Ser	Arg		
545					550					555					560		
Phe	Leu	Ala	Trp	Gly	Glu	Pro	Ala	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu		
				565					570						575		
Ser	Leu	Ala	Leu	Gly	Leu	Val	Leu	Ala	Ala	Leu	Gly	Leu	Phe	Val	His		
			580					585					590				
His	Arg	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly	Gly	Pro	Leu	Ala	Cys		
		595					600					605					
Phe	Gly	Leu	Val	Cys	Leu	Gly	Leu	Val	Cys	Leu	Ser	Val	Leu	Leu	Phe		
	610					615					620						
Pro	Gly	Gln	Pro	Ser	Pro	Ala	Arg	Cys	Leu	Ala	Gln	Gln	Pro	Leu	Ser		
625					630					635					640		
His	Leu	Pro	Leu	Thr	Gly	Cys	Leu	Ser	Thr	Leu	Phe	Leu	Gln	Ala	Ala		
				645					650					655			
Glu	Ile	Phe	Val	Glu	Ser	Glu	Leu	Pro	Leu	Ser	Trp	Ala	Asp	Arg	Leu		
			660					665					670				
Ser	Gly	Cys	Leu	Arg	Gly	Pro	Trp	Ala	Trp	Leu	Val	Val	Leu	Leu	Ala		
		675					680					685					
Met	Leu	Val	Glu	Val	Ala	Leu	Cys	Thr	Trp	Tyr	Leu	Val	Ala	Phe	Pro		
	690					695					700						
Pro	Glu	Val	Val	Thr	Asp	Trp	His	Met	Leu	Pro	Thr	Glu	Ala	Leu	Val		
705					710					715					720		
His	Cys	Arg	Thr	Arg	Ser	Trp	Val	Ser	Phe	Gly	Leu	Ala	His	Ala	Thr		
				725					730					735			
Asn	Ala	Thr	Leu	Ala	Phe	Leu	Cys	Phe	Leu	Gly	Thr	Phe	Leu	Val	Arg		
			740					745					750				
Ser	Gln	Pro	Gly	Cys	Tyr	Asn	Arg	Ala	Arg	Gly	Leu	Thr	Phe	Ala	Met		
		755					760					765					
Leu	Ala	Tyr	Phe	Ile	Thr	Trp	Val	Ser	Phe	Val	Pro	Leu	Leu	Ala	Asn		
	770					775					780						
Val	Gln	Val	Val	Leu	Arg	Pro	Ala	Val	Gln	Met	Gly	Ala	Leu	Leu	Leu		
785					790					795					800		
Cys	Val	Leu	Gly	Ile	Leu	Ala	Ala	Phe	His	Leu	Pro	Arg	Cys	Tyr	Leu		
				805					810					815			
Leu	Met	Arg	Gln	Pro	Gly	Leu	Asn	Thr	Pro	Glu	Phe	Phe	Leu	Gly	Gly		
			820					825					830				

Gly Pro Gly Asp Ala Gln Gly Gln Asn Asp Gly Asn Thr Gly Asn Gln  
835 840 845

Gly Lys His Glu  
850

<210> 16  
<211> 3240  
<212> DNA  
<213> Mus musculus

<220>  
<223> mouse Sac non taster 129 T1R3 sweet taste receptor  
genomic

<400> 16  
acatctgtgg ctccaacccc acacacccat ctattgttag tgctggagac ttctacctac 60  
catgccagct ttggctatca tgggtctcag cctggctgct ttcttgagac ttgggatggg 120  
ggcctctttg tgtctgtcac agcaattcaa ggcacaagg gactacatac tgggcgggct 180  
atttccccctg ggctcgaccg aggaggccac tctcaaccag agagcacaac ccaacagcac 240  
cctgtgtaac aggtatggag gctagtagct ggggtgggag tgaaccgaag cttggcagct 300  
ttggctccgt ggtactacca atctggggaa ggggtgggta tcagtttcca tgtggcctca 360  
ggttctcacc cctcggtttg ttcttgccca tggctatgaa gatggctgtg gaggagatca 420  
acaatggatc tgccttgctc cctgggctgc ggctgggcta tgacctattt gacacatgct 480  
ccgagccagt ggtcaccatg aaatccagtc tcatgttcct ggccaagggtg ggcagtcaaa 540  
gcattgctgc ctactgcaac tacacacagt accaaccctg tgtgctggct gtcactcgcc 600  
cccactcatc agagcttgcc ctctattacag gcaagttctt cagcttcttc ctcatgccac 660  
aggtgagccc acttcctttg tgttctcaac cgattgcacc cattgagctc tcacatcaga 720  
aagtgcctct tgcaccac aggtcagcta tagcgccagc atggatcggc taagtgaccg 780  
ggaaacgttt ccactcctct tccgcacagt gccagtgac cgggtgcagc tgcaggcagt 840  
tgtgactctg ttgcagaact tcagctggaa ctgggtggcc gccttaggga gtgatgatga 900  
ctatggccgg gaaggtctga gcatcttttc tagtctggcc aatgcacgag gtatctgcat 960  
cgcacatgag ggcttggtgc cacaacatga cactagtggc caacagttgg gcaaggtgct 1020  
ggatgtgcta cgccaagtga accaaagtaa agtacaagtg gtgggtgctgt ttgcctctgc 1080  
ccgtgctgtc tactccccctt ttagttacag catccatcat ggctctctac ccaaggtagt 1140  
ggtggccagt gagtcttggc tgacatctga cctggctcat acacttccca atattgcccg 1200  
tgtgggcact gtgcttgggt ttttgacagc ggggtgccta ctgctgaat ttccccatta 1260  
tgtggagact caccttgccc tggccgctga cccagcattc tgtgctcac tgaatgcgga 1320  
gttgatctct gaggaaacatg tgatggggca acgctgtcca cagtgtgacg acatcatgct 1380  
gcagaacctc tcatctgggc tgttgacgaa cctatcagct gggcaattgc accaccaaat 1440  
atttgcaacc tatgcagctg tgtacagtgt ggctcaagcc cttcacaaca ccctacagt 1500  
caatgtctca cattgccacg tatcagaaca tgttctaccc tggcaggtaa gggtaggggt 1560  
ttttgctggg ttttgctgc tcctgcagga aactgaacc aggcagagcc aaatcatgtt 1620  
gtgactggag aggccttacc ctgactccac tccacagctc ctggagaaca tgtacaatat 1680  
gagtttccat gctcgagact tgacactaca gtttgatgct gaaggggaatg tagacatgga 1740  
atatgacctg aagatgtggg tgtggcagag cctaacacct gtattacata ctgtgggcac 1800  
cttcaacggc acccttcagc tgcagcagtc taaaatgtac tggccaggca accaggttaag 1860  
gacaagacag gcaaaaagga tgggtgggtg aagcttgctg gtcttgggccc agtgctagcc 1920  
aaggggaggg ctaacccaag gctccatgtc cagggtgccag tctcccagtg ttcccggcag 1980  
tgcaaatgat gccaggttcg ccgagtaaag ggctttcatt cctgctgcta tgactgctg 2040  
gactgcaagg cgggcagcta ccggaagcat ccaggtgaac cgtcttccct agacagtctg 2100  
cacagccggg ctagggggca gaagcattca agtctggcaa gcgcccctccc gcgggggctaa 2160  
tgtggagaca gttactgtgg gggctggctg gggaggtcgg tctcccatca gcagacccca 2220  
cattactttt ctctcttcca tcactacaga tgacttcacc tgtactccat gtaaccagga 2280  
ccagtggctc ccagagaaaa gcacagcctg cttacctcgc agggcccaagt ttctggcttg 2340  
gggggagcca gttgtgctgt cactcctcct gctgcttgc ctgggtgctg gtctagcact 2400  
ggctgctctg gggctctctg tccaccactg ggacagccct cttgtccagg cctcaggcgg 2460  
ctcacagttc tgccttggcc tgatctgctt aggcctcttc tgcctcagtg tccttctgtt 2520  
cccaggacgg ccaagctctg ccagctgctt tgcacaacaa ccaatggctc acctccctct 2580  
cacaggctgc ctgagcacac tcttctgca agcagctgag accttgtgg agtctgagct 2640

gccactgagc	tgggcaaact	ggctatgcag	ctaccttcgg	ggactctggg	cctggctagt	2700
ggtactgttg	gccacttttg	tggaggcagc	actatgtgcc	tggtatttga	ccgctttccc	2760
accagaggtg	gtgacagact	ggtcagtgct	gcccacagag	gtactggagc	actgccacgt	2820
gcgttcctgg	gtcagcctgg	gcttggtgca	catcaccaat	gcaatgttag	ctttcctctg	2880
ctttctgggc	actttcctgg	tacagagcca	gcctggccgc	tacaaccgtg	cccgtggtct	2940
caccttcgcc	atgctagctt	atttcacac	ctgggtctct	tttgtgcccc	tcctggccaa	3000
tgtgcaggtg	gcctaccagc	cagctgtgca	gatgggtgct	atcctagtct	gtgccctggg	3060
catcctggtc	accttccacc	tgcccaagtg	ctatgtgctt	ctttggctgc	caaagctcaa	3120
cacccaggag	ttcttcctgg	gaaggaatgc	caagaaagca	gcagatgaga	acagtggcgg	3180
tggtgaggca	gctcaggaac	acaatgaatg	accactgacc	cgtgaccttc	ccttttaggga	3240

<210> 17  
 <211> 2577  
 <212> DNA  
 <213> Mus musculus

<220>  
 <223> mouse Sac non taster 129 T1R3 sweet taste receptor  
 CDS

<400> 17						
atgccagctt	tggtatcat	gggtctcagc	ctggctgctt	tcctggagct	tgggatgggg	60
gcctctttgt	gtctgtcaca	gcaattcaag	gcacaagggg	actacatact	gggcgggcta	120
tttcccctgg	gctcgaccga	ggaggccact	ctcaaccaga	gagcacaacc	caacagcacc	180
ctgtgtaaca	ggttctcacc	cctcggtttg	ttcctggcca	tggtatgaa	gatggctgtg	240
gaggagatca	acaatggatc	tgcttgtctc	cctgggctgc	ggctgggcta	tgacctattt	300
gacacatgct	ccgagccagt	ggtcaccatg	aaatccagtc	tcatgttctt	ggccaagggtg	360
ggcagtcaaa	gcattgctgc	ctactgcaac	tacacacagt	accaaccccc	tgtgctggct	420
gtcactggcc	cccactcatc	agagcttgcc	ctcattacag	gcaagtctct	cagcttcttc	480
ctcatgccc	aggtcagcta	tagcgccagc	atggatcggc	taagtgaccg	ggaaacgttt	540
ccatccttct	tcgcacacagt	gcccagtgac	cgggtgcagc	tgcaggcagt	tgtgactctg	600
ttgcagaact	tcagctggaa	ctgggtggcc	gccttaggga	gtgatgatga	ctatggccgg	660
gaaggctctga	gcactctttc	tagtctggcc	aatgcacgag	gtatctgcat	cgcacatgag	720
ggcctgggtgc	cacaacatga	cactagtggc	caacagttgg	gcaagggtgct	ggatgtgcta	780
cgccaagtga	accaaaagtaa	agtacaagtg	gtggtgctgt	ttgcctctgc	ccgtgctgtc	840
tactcccttt	ttagttacag	catccatcat	ggcctctcac	ccaaggatatg	ggtggccagt	900
gagtcttggc	tgacatctga	cctggctcatg	acacttccca	atattgcccg	tgtgggact	960
gtgcttgggt	ttttgcagcg	gggtgcccta	ctgcctgaat	tttcccatta	tgtggagact	1020
caccttgccc	tggccgctga	cccagcatte	tgtgcctcac	tgaatgcgga	gttgatctg	1080
gaggaacatg	tgatggggca	acgctgtcca	cagtgtgacg	acatcatgct	gcagaacctt	1140
tcactctggc	tggtgcagaa	cctatcagct	gggcaattgc	accaccaa	atttgcaacc	1200
tatgcagctg	tgtacagtgt	ggctcaagcc	cttcacaaca	ccctacagtg	caatgtctca	1260
cattgccacg	tatcagaaca	tggtctaccc	tggcagctcc	tggagaacat	gtacaatatg	1320
agtttccatg	ctcgagactt	gacactacag	tttgatgctg	aagggaatgt	agacatggaa	1380
tatgacctga	agatgtgggt	gtggcagagc	cctacacctg	tattacatac	tgtgggcacc	1440
ttcaacggca	cccttcagct	gcagcagctt	aaaatgtact	ggccaggcaa	ccaggtgcca	1500
gtctcccagt	gttcccgcga	gtgcaaagat	ggccagggtc	gccgagtaaa	gggctttcat	1560
tcctgtgctg	atgactgctg	ggactgcaag	gcgggcagct	accggaagca	tccagatgac	1620
ttcactgtga	ctccatgtaa	ccaggaccag	tggtccccag	agaaaagcac	agcctgctta	1680
cctcgcaggc	ccaagtcttct	ggcttggggg	gagccagttg	tgtgtgctact	cctcctgctg	1740
ctttgcctgg	tgtgtgggtct	agcactggct	gctctggggc	tctctgtcca	ccactgggac	1800
agccctcttg	tccaggcctc	aggcggctca	cagttctgct	ttggcctgat	ctgcctaggc	1860
ctcttctgcc	tcagtgtcct	tctgttccca	ggacggccaa	gctctgccag	ctgccttgca	1920
caacaaccaa	tggttcacct	ccctctcaca	ggctgcctga	gcacactctt	cctgcaagca	1980
gctgagacct	ttgtggagtc	tgagctgcca	ctgagctggg	caaactggct	atgcagctac	2040
cttcggggag	tctgggcctg	gctagtggta	ctgttgggca	cttttggtga	ggcagcacta	2100
tgtgctgggt	atttgaccgc	tttcccacca	gaggtgggtga	cagactgggtc	agtgtgccc	2160
acagaggtag	tgagcactg	ccacgtgcgt	tcctgggtca	gcctgggctt	ggtgcacatc	2220
accaatgcaa	tgttagcttt	cctctgcttt	ctgggcactt	tcctggtaca	gagccagcct	2280
ggccgctaca	accgtgcccc	tggtctcacc	ttcgccatgc	tagcttattt	catcacctgg	2340

gtctcttttg tgccctcctt ggccaatgtg caggtggcct accagccagc tgtgcagatg 2400  
 ggtgctatcc tagtctgtgc cctgggcatc ctgggtcacct tccacctgcc caagtgtat 2460  
 gtgcttcttt ggctgccaag gctcaacacc caggagttct tctgggaag gaatgccaag 2520  
 aaagcagcag atgagaacag tggcgggtgt gaggcagctc aggaacacaa tgaatga 2577

<210> 18  
 <211> 858  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> mouse Sac non taster 129 T1R3 sweet taste receptor

<400> 18  
 Met Pro Ala Leu Ala Ile Met Gly Leu Ser Leu Ala Ala Phe Leu Glu  
 1 5 10 15  
 Leu Gly Met Gly Ala Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln  
 20 25 30  
 Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu  
 35 40 45  
 Ala Thr Leu Asn Gln Arg Ala Gln Pro Asn Ser Thr Leu Cys Asn Arg  
 50 55 60  
 Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val  
 65 70 75 80  
 Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly  
 85 90 95  
 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser  
 100 105 110  
 Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr  
 115 120 125  
 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro  
 130 135 140  
 His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe  
 145 150 155 160  
 Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp  
 165 170 175  
 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val  
 180 185 190  
 Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp  
 195 200 205  
 Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser  
 210 215 220  
 Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu  
 225 230 235 240

Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val	245	250	255
Leu	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val	260	265	270
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile	275	280	285
His	His	Gly	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu	290	295	300
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr	305	310	315
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His	325	330	335
Tyr	Val	Glu	Thr	His	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Ala	Phe	Cys	Ala	340	345	350
Ser	Leu	Asn	Ala	Glu	Leu	Asp	Leu	Glu	Glu	His	Val	Met	Gly	Gln	Arg	355	360	365
Cys	Pro	Gln	Cys	Asp	Asp	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu	370	375	380
Leu	Gln	Asn	Leu	Ser	Ala	Gly	Gln	Leu	His	His	Gln	Ile	Phe	Ala	Thr	385	390	395
Tyr	Ala	Ala	Val	Tyr	Ser	Val	Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln	405	410	415
Cys	Asn	Val	Ser	His	Cys	His	Val	Ser	Glu	His	Val	Leu	Pro	Trp	Gln	420	425	430
Leu	Leu	Glu	Asn	Met	Tyr	Asn	Met	Ser	Phe	His	Ala	Arg	Asp	Leu	Thr	435	440	445
Leu	Gln	Phe	Asp	Ala	Glu	Gly	Asn	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys	450	455	460
Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr	465	470	475
Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	Gln	Ser	Lys	Met	Tyr	Trp	Pro	Gly	485	490	495
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln	500	505	510
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	515	520	525
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr	530	535	540
Pro	Cys	Asn	Gln	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Ala	Cys	Leu	545	550	555

Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Val Val Leu Ser  
                     565                    570                    575  
 Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu Ala Ala Leu  
                     580                    585                    590  
 Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln Ala Ser Gly  
                     595                    600                    605  
 Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu  
                     610                    615                    620  
 Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser Cys Leu Ala  
                     625                    630                    635                    640  
 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu  
                     645                    650                    655  
 Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser  
                     660                    665                    670  
 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu  
                     675                    680                    685  
 Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr  
                     690                    695                    700  
 Leu Thr Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro  
                     705                    710                    715                    720  
 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly  
                     725                    730                    735  
 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly  
                     740                    745                    750  
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly  
                     755                    760                    765  
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val  
                     770                    775                    780  
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met  
                     785                    790                    795                    800  
 Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu  
                     805                    810                    815  
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu  
                     820                    825                    830  
 Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly  
                     835                    840                    845  
 Gly Gly Glu Ala Ala Gln Glu His Asn Glu  
                     850                    855



<210> 19  
 <211> 2577  
 <212> DNA  
 <213> Mus musculus

<220>  
 <223> mouse Sac taster SWR T1R3 sweet taste receptor CDS

<400> 19  
 atgccagctt tggctatcat gggctctcage ctggctgctt tcctggagct tgggatgggg 60  
 gcctctttgt gtctgtcaca gcaattcaag gcacaagggg actacatact gggcgggcta 120  
 tttcccttg gctcaaccga ggaggccact ctcaaccaga gaacacaacc caacagcatc 180  
 ctgtgtaaca ggttctcacc cctcgggttg ttcctggcca tggctatgaa gatggctgtg 240  
 gaggagatca acaatggatc tgccttgctc cctgggctgc ggctgggcta tgacctatct 300  
 gacacatgct ccgagccagt ggtcaccatg aaatccagtc tcatgttctt ggccaagggtg 360  
 ggcagtcaaa gcattgctgc ctactgcaac tacacacagt accaaccctg tgtgctggct 420  
 gtcactggcc cccactcatc agagcttgcc ctcatcagag gcaagttctt cagcttcttc 480  
 ctcatgccac aggtcagcta tagcgccagc atggatcggc taagtgaccg ggaaacgttt 540  
 ccactcttct tccgcacagt gcccagtgac cgggtgcagc tgcaggcagt tgtgactctg 600  
 ttgcagaact tcagctggaa ctgggtggcc gccttaggga gtgatgatga ctatggcccg 660  
 gaaggctctga gcatcttttc tagtctggcc aatgcacgag gtatctgcat cgcacatgag 720  
 ggcttgggtg cacaacatga cactagtggc caacagttgg gcaagggtgt ggatgtgcta 780  
 tgccaagtga accaaagtaa agtacaagtg gtggtgctgt ttgcctctgc ccgtgctgtc 840  
 tactcccttt ttagttacag catccatcat ggcctctcac ccaaggatatg ggtggccagt 900  
 gagtcttggc tgacatctga cctggctcatg acacttccca atattgcccg tgtgggcact 960  
 gtgcttgggt ttttgacgag ggggtgccct ctgcctgaat tttccatta tgtggagact 1020  
 caccttgccc tggccgctga cccagcatc tgtgcctcac tgaatgcgga gttggatctg 1080  
 gaggaacatg tgatggggca acgctgtcca cagtgtgacg acatcatgct gcagaacct 1140  
 tcatctgggc tgttgacaga cctatcagct gggcaattgc accaccaaat atttgcaacc 1200  
 tatgcagctg tgtacagtgt ggtcgaagcc cttcacaaca ccctacagtg caatgtctca 1260  
 cattgccatg tatcagaaca tgttctacc tggcagctcc tggagaacat gtacaatatg 1320  
 agtttccatg ctcgagactt gacactacag ttgtatgctg aagggaatgt agacatggaa 1380  
 tatgacctga agatgtgggt gtggcagagc cctacacctg tattacatac tgtgggcacc 1440  
 ttcaacggca cccttcagct gcagcagctt aaaatgtact ggccaggcaa ccagggtgcca 1500  
 gtctcccagt gttcccggca gtgcaaagat ggccagggtc gccagtaaaa gggctttcat 1560  
 tcctgctgct atgactgctg ggactgcaag gcgggcagct accggaagca tccagatgac 1620  
 ttcacctgta ctccatgtaa ccaggaccag tggctcccag agaaaagcac agcctgctta 1680  
 cctcgacagg ccaagtttct ggcttggggg gagccagttg tgcctgctact cctcctgctg 1740  
 ctttgccctg tgcctgggtc agcactggct gctctggggc tctctgtcca ccactgggac 1800  
 agccctcttg tccaggcctc aggcggctca cagttctgct ttggcctgat ctgcctaggc 1860  
 ctctctgccc tcagtgtcct tctgttccca ggacggccaa gctctgccag ctgccttgca 1920  
 caacaaccaa tggctcacct ccctctcaca ggctgctga gcacactctt cctgcaagca 1980  
 gctgagacct ttgtggagtc tgagctgcca ctgagctggg caaactggct atgcagctac 2040  
 cttcggggac tctgggcctg gctagtggta ctgtcggcca cttttgtgga ggcagcacta 2100  
 tgtgcctggt atttgaccgc tttcccacca gaggtggtga cagactgggtc agtgctgccc 2160  
 acagaggtag tggagcactg ccacgtgcgt tcctgggtca gcctgggctt ggtgcacatc 2220  
 accaatgcaa tgttagcttt cctctgcttt ctgggcactt tcctgggtaca gagccagcct 2280  
 ggccgctaca accgtgcccg tggctctcac ttcgccatgc tagcttattt catcacctgg 2340  
 gtctcttttg tgccctcctt ggccaatgtg cagggtggcct accagccagc tgtgcagatg 2400  
 ggtgctatcc tagtctgtgc cctgggcac cctgggtcac tccacctgcc caagtgtat 2460  
 gtgcttcttt ggctgcaaaa gctcaacacc caggagttct tcctgggaag gaatgccaa 2520  
 aaagcagcag atgagaacag tggcgggtgt gaggcagctc aggaacacaa tgaatga 2577

<210> 20  
 <211> 858  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> mouse Sac taster SWR T1R3 sweet taste receptor

<400> 20

Met	Pro	Ala	Leu	Ala	Ile	Met	Gly	Leu	Ser	Leu	Ala	Ala	Phe	Leu	Glu	1	5	10	15
Leu	Gly	Met	Gly	Ala	Ser	Leu	Cys	Leu	Ser	Gln	Gln	Phe	Lys	Ala	Gln	20	25	30	
Gly	Asp	Tyr	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Ser	Thr	Glu	Glu	35	40	45	
Ala	Thr	Leu	Asn	Gln	Arg	Thr	Gln	Pro	Asn	Ser	Ile	Leu	Cys	Asn	Arg	50	55	60	
Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val	65	70	75	80
Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly	85	90	95	
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Ser	100	105	110	
Ser	Leu	Met	Phe	Leu	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr	115	120	125	
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro	130	135	140	
His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe	145	150	155	160
Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp	165	170	175	
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val	180	185	190	
Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp	195	200	205	
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser	210	215	220	
Ile	Phe	Ser	Ser	Leu	Ala	Asn	Ala	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu	225	230	235	240
Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val	245	250	255	
Leu	Asp	Val	Leu	Cys	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val	260	265	270	
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile	275	280	285	
His	His	Gly	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu	290	295	300	
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr	305	310	315	320

Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His  
 325 330 335  
 Tyr Val Glu Thr His Leu Ala Leu Ala Ala Asp Pro Ala Phe Cys Ala  
 340 345 350  
 Ser Leu Asn Ala Glu Leu Asp Leu Glu Glu His Val Met Gly Gln Arg  
 355 360 365  
 Cys Pro Gln Cys Asp Asp Ile Met Leu Gln Asn Leu Ser Ser Gly Leu  
 370 375 380  
 Leu Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr  
 385 390 395 400  
 Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln  
 405 410 415  
 Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln  
 420 425 430  
 Leu Leu Glu Asn Met Tyr Asn Met Ser Phe His Ala Arg Asp Leu Thr  
 435 440 445  
 Leu Gln Phe Asp Ala Glu Gly Asn Val Asp Met Glu Tyr Asp Leu Lys  
 450 455 460  
 Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr  
 465 470 475 480  
 Phe Asn Gly Thr Leu Gln Leu Gln Gln Ser Lys Met Tyr Trp Pro Gly  
 485 490 495  
 Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln  
 500 505 510  
 Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp  
 515 520 525  
 Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr  
 530 535 540  
 Pro Cys Asn Gln Asp Gln Trp Ser Pro Glu Lys Ser Thr Ala Cys Leu  
 545 550 555 560  
 Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Val Val Leu Ser  
 565 570 575  
 Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu Ala Ala Leu  
 580 585 590  
 Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln Ala Ser Gly  
 595 600 605  
 Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu  
 610 615 620  
 Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser Cys Leu Ala  
 625 630 635 640

Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu  
                     645                    650                    655  
 Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser  
                     660                    665                    670  
 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu  
                     675                    680                    685  
 Val Val Leu Ser Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr  
                     690                    695                    700  
 Leu Thr Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro  
 705                    710                    715                    720  
 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly  
                     725                    730                    735  
 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly  
                     740                    745                    750  
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly  
                     755                    760                    765  
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val  
                     770                    775                    780  
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met  
 785                    790                    795                    800  
 Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu  
                     805                    810                    815  
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu  
                     820                    825                    830  
 Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly  
                     835                    840                    845  
 Gly Gly Glu Ala Ala Gln Glu His Asn Glu  
                     850                    855

<210> 21

<211> 3200

<212> DNA

<213> Mus musculus

<220>

<223> mouse Sac taster C57 T1R3 sweet taste receptor  
genomic

<400> 21

cccacacacc caccattgt tagtgctgga gacttctacc taccatgccca gctttggcta 60  
 tcatgggtct cagcctggct gctttcctgg agcttgggat gggggcctct ttgtgtctgt 120  
 cacagcaatt caaggcaca ggggactaca tactgggcgg gctatttccc ctgggctcaa 180  
 ccgaggaggc cactctcaac cagagaacac aaccaacag catcccgatg aacaggtatg 240  
 gaggctagta gctgggggtg gagtgaaccg aagcttggca gctttggctc cgtggtacta 300  
 ccaatctggg aagagggtgt gatcagtttc catgtggcct caggttctca ccccttggtt 360  
 tgttctctgg catggctatg aagatggctg tggaggagat caacaatgga tctgccttgc 420  
 tccctgggct gcggctgggc tatgacctat ttgacacatg ctccgagcca gtggtcacca 480

tgaaatccag	tctcatgttc	ctggccaagg	tgggcagtc	aagcattgct	gcctactgca	540
actacacaca	gtaccaaccc	cgtgtgctgg	ctgtcatcgg	ccccactca	tcagagcttg	600
ccctcattac	aggcaagttc	ttcagcttct	tcctcatgcc	acaggtgagc	ccacttcctt	660
tgtgtttctca	accgattgca	cccattgagc	tctcatatca	gaaagtgctt	cttgatcacc	720
acaggtcagc	tatagtgcc	gcatggatcg	gctaagtga	cgggaaacgt	ttccatcctt	780
cttccgcaca	gtgccagtg	accgggtgca	gctgcaggca	gttgtgactc	tggtgcagaa	840
cttcagctgg	aactgggtgg	ccgccttagg	gagtgatgat	gactatggcc	gggaaggtct	900
gagcatcttt	tctagtctgg	ccaatgcacg	aggtatctgc	atcgcacatg	agggcctggt	960
gccacaacat	gacactagt	gccaacagtt	gggcaaggtg	ctggatgtac	tacgccaaagt	1020
gaaccaaagt	aaagtacaag	tggtggtgct	gtttgcctct	gcccgtgctg	tctactccct	1080
ttttagttac	agcatccatc	atggcctctc	acccaaggta	tgggtggcca	gtgagtcttg	1140
gctgacatct	gacctgggtc	tgacacttcc	caatatggcc	cgtgtgggca	ctgtgcttgg	1200
gtttttgcag	cggggtgccc	tactgcctga	attttcccat	tatgtggaga	ctcaccttgc	1260
cctggccgct	gacccagcat	tctgtgcctc	actgaatgcg	gagttggatc	tggaggaaca	1320
tgtgatgggg	caacgctgtc	cacgggtgtg	cgacatcatg	ctgcagaacc	tatcatctgg	1380
gctgtttgcag	aacctatcag	ctgggcaatt	gcaccaccaa	atatttgcaa	cctatgcagc	1440
tgtgtacagt	gtggctcaag	cccttcacaa	caccctacag	tgcaatgtct	cacattgcca	1500
cgtatcagaa	catgtttctac	cctggcaggt	aagggtaggg	ttttttgctg	ggttttgcct	1560
gctcctgcag	gaacactgaa	ccaggcagag	ccaaatcttg	ttgtgactgg	agaggcctta	1620
ccctgactcc	actccacagc	tcctggagaa	catgtacaat	atgagtttcc	atgctcgaga	1680
cttgacacta	cagtttgatg	ctgaaggga	tgtagacatg	gaatatgacc	tgaagatgtg	1740
gggtgtgcag	agccctacac	ctgtattaca	tactgtgggc	accttcaacg	gcaccttca	1800
gctgcagcag	tctaaaatgt	actggccagg	caaccaggta	aggacaagac	aggcaaaaaag	1860
gatgggtgggt	agaagcttgt	cggctcttggg	ccagtgtctag	ccaaggggag	gcctaaccga	1920
aggctccatg	tacaggtgcc	agtctcccag	tggtcccggc	agtgcagaag	tggccaggtt	1980
cgccgagtaa	agggtcttca	ttcctgctgc	tatgactgcg	tggactgcaa	ggcgggcagc	2040
taccggaagc	atccaggtga	accgtcttcc	ctagacagtc	tgcacagccg	ggctaggggg	2100
cagaagcatt	caagtctggc	aagcgccctc	ccgcggggct	aatgtggaga	cagttactgt	2160
gggggctggc	tggggagggtc	ggtctcccat	cagcagacc	cacattactt	ttcttccttc	2220
catcactaca	gatgacttca	cctgtactcc	atgtaaccag	gaccagtggg	ccccagagaa	2280
aagcacagcc	tgcttacctc	gcaggcccaa	gtttctggct	tgggggggagc	cagtttgtgt	2340
gtcactcctc	ctgctgcttt	gcctgggtgct	gggtctagca	ctgggtgctc	tggggctctc	2400
tgtccaccac	tgggacagcc	ctcttgtcca	ggcctcaggt	ggctcacagt	tctgcttttg	2460
cctgatctgc	ctaggcctct	tctgcctcag	tgctcttctg	ttcccagggc	ggccaagctc	2520
tgccagctgc	cttgacacac	aaccaatggc	tcacctccct	ctcacaggct	gcctgagcac	2580
actcttctctg	caagcagctg	agacctttgt	ggagtctgag	ctgccactga	gctggggcaaa	2640
ctggctatgc	agctaccttc	ggggactctg	ggcctggcta	gtgggtactgt	tggccacttt	2700
tgtggaggca	gcactatgtg	cctgggtattt	gategcttct	ccaccagagg	tgggtgacaga	2760
ctggctcagtg	ctgcccacag	aggtactgga	gcactgccac	gtgcgttcc	gggtcagcct	2820
gggcttgggtg	cacatcacca	atgcaatggt	agctttcctc	tgctttctgg	gcactttcct	2880
ggtacagagc	cagcctggcc	gctacaaccg	tgcccggtgt	ctcaccttcg	ccatgctagc	2940
ttatttcatc	acctgggtct	cttttgtgcc	cctcctggcc	aatgtgcagg	tggcctacca	3000
gccagctgtg	cagatgggtg	ctatcctagt	ctgtgcctg	ggcatcctgg	tcaccttcca	3060
cctgcccag	tgctatgtgc	ttctttggct	gccaaagctc	aacaccagag	agttcttctc	3120
gggaaggaat	gccaaagaaag	cagcagatga	gaacagtggc	ggtggtgagg	cagctcaggg	3180
acacaatgaa	tgaccactga					3200

<210> 22  
 <211> 2577  
 <212> DNA  
 <213> Mus musculus

<220>  
 <223> mouse Sac taster C57 T1R3 sweet taste receptor CDS

<400> 22	
atgccagctt	tggctatcat
gcctctttgt	gtctgtcaca
tttcccctgg	gtcacaaccga
ccgtgcaaca	gggttctcacc
gggtctcagc	ctggctgctt
gcacaagggg	actacatact
ctcaaccaga	gaacacaacc
tggtatgaa	gatggctgtg
gggtctcagc	ctggctgctt
gcacaagggg	actacatact
ctcaaccaga	gaacacaacc
tggtatgaa	gatggctgtg
gggtctcagc	ctggctgctt
gcacaagggg	actacatact
ctcaaccaga	gaacacaacc
tggtatgaa	gatggctgtg

```

gaggagatca acaatggatc tgccttgctc cctgggctgc ggctgggcta tgacctat 300
gacacatgct ccgagccagt ggtcaccatg aaatccagtc tcatgttctt ggccaagg 360
ggcagtc aaa gcaattgctgc ctactgcaac tacacacagt accaaccctt tgtgctgg 420
gtcatcgccc cccactcatc agagcttgcc ctcatcag gcaagttctt cagcttct 480
ctcatgccac aggtcagcta tagtgccagc atggatcggc taagtgaacc ggaaacgt 540
ccatccttct tccgcacagt gcccagtgac cgggtgcagc tgcaggcagt tgtgactc 600
ttgcagaact tcagctggaa ctgggtggcc gccttaggga gtgatgatga ctatggcc 660
gaaggtctga gcatcttttc tagtctggcc aatgcacgag gtatctgcat cgcacatg 720
ggcctgggtg cacaacatga cactagtggc caacagttgg gcaaggtgct ggatgtact 780
cgccaagtga accaaagtaa agtacaagtg gtgggtgctg ttgcctctgc ccgtgctg 840
tactcccttt ttagttacag catccatcat ggccctctac ccaaggtatg ggtggccag 900
gagtcttggc tgacatctga cctgggtcat acacttccca atattgccc tgtgggcact 960
gtgcttgggt ttttgacagc ggtgccccta ctgcctgaat tttccatta tgtggagact 1020
caccttgccc tggccgctga cccagcattc tgtgcctcac tgaatgcgga gttggatc 1080
gaggaacatg tgatggggca acgctgtcca cgggtgtgac acatcatgct gcagaac 1140
tcactctggc tgttgacaga cctatcagct gggcaattgc accaccaa atttgcaac 1200
tatgcagctg tgtacagtgt ggctcaagcc cttcacaaca ccctacagt caatgtct 1260
cattgccacg tatcagaaca tgttctaccc tggcagctcc tggagaacat gtacaatat 1320
agtttccatg ctgcagactt gacactacag tttgatgctg aagggaatgt agacatgg 1380
tatgacctga agatgtgggt gtggcagagc cctacacctg tattacatac tgtgggc 1440
ttcaacggca ccttcagct gcagcagctt aaaaatgtact ggccaggcaa ccaggtgc 1500
gtctcccagt gttcccgcga gtgcaaagat ggccagggtt gccagtaaa gggctt 1560
tcctgctgct atgactgcgt ggactgcaag ggggagct accggaagca tccagatg 1620
ttcacctgta ctccatgtaa ccaggaccag tggctcccag agaaaagcac agcctg 1680
cctcgcaggc ccaagtttct ggcttggggg gagccagttg tgctgtcact cctcctg 1740
ctttgcctgg tgcctgggtc agcactggct gctctggggc tctctgtcca ccactgg 1800
agccctcttg tccaggcctc aggtgggtca cagttctgct ttggcctgat ctgcctag 1860
ctcttctgcc tcagtgtcct tctgttccca gggcgcccaa gctctgccag ctgccttg 1920
caacaaccaa tggctcacct cctctcaca ggctgctga gcacactctt cctgcaag 1980
gctgagacct ttgtggagtc tgagctgcca ctgagctggg caaactggct atgcagct 2040
cttcggggac tctgggcctg gctagtggta ctgttgcca cttttgtgga ggcagcact 2100
tgtgcctggg atttgatcgc tttccacca gaggtgggtg cagactgggt agtgctgccc 2160
acagaggtac tggagcactg ccacgtgcgt tcttgggtca gcctgggctt ggtgcacat 2220
accaatgcaa tgttagcttt cctctgcttt ctgggcactt tcttgggtaca gagccagc 2280
ggccgctaca accgtgcccg tggctctacc ttcgccatgc tagcttattt catcacct 2340
gtctcttttg tgccctcct ggccaatgtg caggtggcct accagccagc tgtgcagat 2400
ggtgctatcc tagtctgtgc cctgggcctc ctgggtcacct tccacctgcc caagtgc 2460
gtgcttcttt ggctgccaaa gctcaacacc caggagttct tcttgggaag gaatgcc 2520
aaagcagcag atgagaacag tggcgggtgt gaggcagctc agggacacaa tgaatga 2577

```

<210> 23  
 <211> 858  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> mouse Sac taster C57 T1R3 sweet taste receptor

<400> 23  
 Met Pro Ala Leu Ala Ile Met Gly Leu Ser Leu Ala Ala Phe Leu Glu  
 1 5 10 15  
 Leu Gly Met Gly Ala Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln  
 20 25 30  
 Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu  
 35 40 45  
 Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Ser Ile Pro Cys Asn Arg  
 50 55 60

Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val	65	70	75				80
Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly		85	90				95
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Ser	100		105				110
Ser	Leu	Met	Phe	Leu	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr	115		120				125
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro	130		135				140
His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe	145		150				155
Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp		165	170				175
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val		180	185				190
Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp		195	200				205
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser	210		215				220
Ile	Phe	Ser	Ser	Leu	Ala	Asn	Ala	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu	225		230				235
Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val		245	250				255
Leu	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val		260	265				270
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile		275	280				285
His	His	Gly	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu	290		295				300
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr	305		310				315
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His		325	330				335
Tyr	Val	Glu	Thr	His	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Ala	Phe	Cys	Ala		340	345				350
Ser	Leu	Asn	Ala	Glu	Leu	Asp	Leu	Glu	Glu	His	Val	Met	Gly	Gln	Arg		355	360				365
Cys	Pro	Arg	Cys	Asp	Asp	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu	370		375				380

Leu	Gln	Asn	Leu	Ser	Ala	Gly	Gln	Leu	His	His	Gln	Ile	Phe	Ala	Thr	
385					390					395					400	
Tyr	Ala	Ala	Val	Tyr	Ser	Val	Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln	
				405					410					415		
Cys	Asn	Val	Ser	His	Cys	His	Val	Ser	Glu	His	Val	Leu	Pro	Trp	Gln	
			420					425					430			
Leu	Leu	Glu	Asn	Met	Tyr	Asn	Met	Ser	Phe	His	Ala	Arg	Asp	Leu	Thr	
		435					440					445				
Leu	Gln	Phe	Asp	Ala	Glu	Gly	Asn	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys	
	450					455					460					
Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr	
465					470					475					480	
Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	Gln	Ser	Lys	Met	Tyr	Trp	Pro	Gly	
				485					490					495		
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln	
			500					505					510			
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	
		515					520					525				
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr	
	530					535					540					
Pro	Cys	Asn	Gln	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Ala	Cys	Leu	
545					550					555					560	
Pro	Arg	Arg	Pro	Lys	Phe	Leu	Ala	Trp	Gly	Glu	Pro	Val	Val	Leu	Ser	
				565					570					575		
Leu	Leu	Leu	Leu	Leu	Cys	Leu	Val	Leu	Gly	Leu	Ala	Leu	Ala	Ala	Leu	
			580					585					590			
Gly	Leu	Ser	Val	His	His	Trp	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly	
		595					600					605				
Gly	Ser	Gln	Phe	Cys	Phe	Gly	Leu	Ile	Cys	Leu	Gly	Leu	Phe	Cys	Leu	
	610					615					620					
Ser	Val	Leu	Leu	Phe	Pro	Gly	Arg	Pro	Ser	Ser	Ala	Ser	Cys	Leu	Ala	
625					630					635					640	
Gln	Gln	Pro	Met	Ala	His	Leu	Pro	Leu	Thr	Gly	Cys	Leu	Ser	Thr	Leu	
				645					650					655		
Phe	Leu	Gln	Ala	Ala	Glu	Thr	Phe	Val	Glu	Ser	Glu	Leu	Pro	Leu	Ser	
			660					665					670			
Trp	Ala	Asn	Trp	Leu	Cys	Ser	Tyr	Leu	Arg	Gly	Leu	Trp	Ala	Trp	Leu	
		675					680					685				
Val	Val	Leu	Leu	Ala	Thr	Phe	Val	Glu	Ala	Ala	Leu	Cys	Ala	Trp	Tyr	
	690					695					700					



Leu Ile Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro  
 705 710 715 720  
 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly  
 725 730 735  
 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly  
 740 745 750  
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly  
 755 760 765  
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val  
 770 775 780  
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met  
 785 790 795 800  
 Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu  
 805 810 815  
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu  
 820 825 830  
 Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly  
 835 840 845  
 Gly Gly Glu Ala Ala Gln Gly His Asn Glu  
 850 855

<210> 24  
 <211> 2577  
 <212> DNA  
 <213> Rattus sp.

<220>  
 <223> rat T1R3 sweet taste receptor CDS

<400> 24  
 atgccggggtt tggctatctt gggcctcagt ctggctgott tcctggagct tgggatgggg 60  
 tcctctttgt gtctgtcaca gcaattcaag gcacaagggg actatatatt ggggtggacta 120  
 tttcccttg gcaacaactga ggaggccact ctcaaccaga gaacacagcc caacggcatc 180  
 ctatgtacca ggttctcgcc ccttggtttg ttcctggcca tggctatgaa gatggctgta 240  
 gaggagatca acaatggatc tgccttgctc cctgggctgc gactgggcta tgacctgtt 300  
 gacacatgct cagagccagt ggtcaccatg aagcccagcc tcatgttcat ggccaagggtg 360  
 ggaagtcaaa gcattgctgc ctactgcaac tacacacagt accaaccctg tgtgctggct 420  
 gtcattgggc cccactcatc agagcttgcc ctcatcagc gcaagtctt cagcttcttc 480  
 ctcatggcac aggtcagcta tagtgccagc atggatcggc taagtgaccg ggaaacattt 540  
 ccataccttct tccgcacagt gccagtgac cgggtgcagc tgcaggccgt tgtgacactg 600  
 ttgcagaatt tcagctggaa ctgggtggct gccttaggta gtgatgatga ctatggccgg 660  
 gaaggtctga gcattctttc tggcttgccc aactcacgag gtatctgcat tgcacacgag 720  
 ggcctgggtgc cacaacatga cactagtggc caacaattgg gcaaggtggg ggatgtgcta 780  
 cgccaagtga accaaagcaa agtacagggtg gtggtgctgt ttgcatctgc ccgtgctgtc 840  
 tactcccttt ttagctacag catccttcat gacctctcac ccaaggatatg ggtggccagt 900  
 gagtccctggc tgacctctga cctgggtcatg acacttccca atattgccc tgtgggcact 960  
 gttcttgggt ttctgcagcg cggtgcccta ctgcctgaat tttccatta tgtggagact 1020  
 cgccctggcc tagctgctga cccaacattc tgtgcctccc tgaaagctga gttggatctg 1080  
 gaggagcgcg tgatggggcc acgctgttca caatgtgact acatcatgct acagaacctg 1140  
 tcatctgggc tgatgcagaa cctatcagct gggcagttgc accaccaaat atttgcaacc 1200  
 tatgcagctg tgtacagtgt ggctcaggcc cttcacaaca ccctgcagt caatgtctca 1260

```

cattgccaca catcagagcc tgttcaaccc tggcagctcc tggagaacat gtacaatatg 1320
agttttccgtg ctccgagactt gacactgcag tttgatgcc aagggagtgt agacatggaa 1380
tatgacctga agatgtgggt gtggcagagc cctacacctg tactacatac tgtaggcacc 1440
ttcaacggca cccttcagct gcagcactcg aaaatgtatt ggccaggcaa ccagggtgcc 1500
gtctccaggt gctcccgga gtgcaaagat ggccagggtgc gcagagtaaa gggctttcat 1560
tcctgctgct atgactgtgt ggactgcaag gcagggagct accggaagca tccagatgac 1620
ttcacctgta ctccatgttg caaggatcag tgggtcccccag aaaaaagcac aacctgctta 1680
cctcgcaggc ccaagtttct ggcttggggg gagccagctg tgctgtcact tctcctgctg 1740
ctttgcctgg tgctgggcct gacactggct gccctggggc tctttgtcca ctactgggac 1800
agccctcttg ttcaggcctc aggtgggtca ctgttctgct ttggcctgat ctgcctaggc 1860
ctcttctgcc tcagtgtcct tctgttccca ggacgaccac gctctgccag ctgccttgcc 1920
caacaaccaa tggctcacct ccctctcaca ggctgcctga gcacactctt cctgcaagca 1980
gccgagatct ttgtggagtc tgagctgcca ctgagttggg caaactggct ctgcagctac 2040
cttcggggcc cctgggcttg gctgggtgta ctgctggcca ctcttgtgga ggctgcacta 2100
tgtgcctggt acttgatggc tttccctcca gaggtgggtga cagattggca ggtgctgccc 2160
acggaggtac tggaaactgc ccgcattgct tcctgggtca gcctgggctt ggtgcacatc 2220
accaatgcag tgtagcttt cctctgcttt ctgggcactt tcctgggtaca gagccagcct 2280
ggctgcctata accgtgcccc tggcctcacc ttcgccatgc tagcttattt catcatctgg 2340
gtctcttttg tgcccctcct ggctaattgt caggtggcct accagccagc tgtgcagatg 2400
ggtgctatct tattctgtgc cctgggcac ctggccacct tccacctgcc caaatgctat 2460
gtacttctgt ggctgccaga gctcaacacc caggagtctt tcctgggaag gagccccaag 2520
gaagcatcag atgggaatag tggtagtagt gaggcaactc ggggacacag tgaatga 2577

```

<210> 25  
 <211> 858  
 <212> PRT  
 <213> Rattus sp.

<220>  
 <223> rat T1R3 sweet taste receptor

<400> 25

Met	Pro	Gly	Leu	Ala	Ile	Leu	Gly	Leu	Ser	Leu	Ala	Ala	Phe	Leu	Glu
1				5					10					15	
Leu	Gly	Met	Gly	Ser	Ser	Leu	Cys	Leu	Ser	Gln	Gln	Phe	Lys	Ala	Gln
			20					25					30		
Gly	Asp	Tyr	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Thr	Thr	Glu	Glu
		35					40					45			
Ala	Thr	Leu	Asn	Gln	Arg	Thr	Gln	Pro	Asn	Gly	Ile	Leu	Cys	Thr	Arg
	50					55					60				
Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val
65					70				75					80	
Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly
			85						90					95	
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Pro
		100						105					110		
Ser	Leu	Met	Phe	Met	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr
		115					120					125			
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro
	130					135						140			

His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe	145	150	155	160
Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp	165	170	175	
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val	180	185	190	
Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp	195	200	205	
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser	210	215	220	
Ile	Phe	Ser	Gly	Leu	Ala	Asn	Ser	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu	225	230	235	240
Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val	245	250	255	
Val	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val	260	265	270	
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile	275	280	285	
Leu	His	Asp	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu	290	295	300	
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr	305	310	315	320
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His	325	330	335	
Tyr	Val	Glu	Thr	Arg	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Thr	Phe	Cys	Ala	340	345	350	
Ser	Leu	Lys	Ala	Glu	Leu	Asp	Leu	Glu	Glu	Arg	Val	Met	Gly	Pro	Arg	355	360	365	
Cys	Ser	Gln	Cys	Asp	Tyr	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu	370	375	380	
Met	Gln	Asn	Leu	Ser	Ala	Gly	Gln	Leu	His	His	Gln	Ile	Phe	Ala	Thr	385	390	395	400
Tyr	Ala	Ala	Val	Tyr	Ser	Val	Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln	405	410	415	
Cys	Asn	Val	Ser	His	Cys	His	Thr	Ser	Glu	Pro	Val	Gln	Pro	Trp	Gln	420	425	430	
Leu	Leu	Glu	Asn	Met	Tyr	Asn	Met	Ser	Phe	Arg	Ala	Arg	Asp	Leu	Thr	435	440	445	
Leu	Gln	Phe	Asp	Ala	Lys	Gly	Ser	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys	450	455	460	

Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr	465	470	475	480
Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	His	Ser	Lys	Met	Tyr	Trp	Pro	Gly	485	490		495
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln	500	505		510
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	515	520		525
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr	530	535		540
Pro	Cys	Gly	Lys	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Thr	Cys	Leu	545	550	555	560
Pro	Arg	Arg	Pro	Lys	Phe	Leu	Ala	Trp	Gly	Glu	Pro	Ala	Val	Leu	Ser	565	570		575
Leu	Leu	Leu	Leu	Leu	Cys	Leu	Val	Leu	Gly	Leu	Thr	Leu	Ala	Ala	Leu	580	585		590
Gly	Leu	Phe	Val	His	Tyr	Trp	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly	595	600		605
Gly	Ser	Leu	Phe	Cys	Phe	Gly	Leu	Ile	Cys	Leu	Gly	Leu	Phe	Cys	Leu	610	615	620	
Ser	Val	Leu	Leu	Phe	Pro	Gly	Arg	Pro	Arg	Ser	Ala	Ser	Cys	Leu	Ala	625	630	635	640
Gln	Gln	Pro	Met	Ala	His	Leu	Pro	Leu	Thr	Gly	Cys	Leu	Ser	Thr	Leu	645	650		655
Phe	Leu	Gln	Ala	Ala	Glu	Ile	Phe	Val	Glu	Ser	Glu	Leu	Pro	Leu	Ser	660	665		670
Trp	Ala	Asn	Trp	Leu	Cys	Ser	Tyr	Leu	Arg	Gly	Pro	Trp	Ala	Trp	Leu	675	680		685
Val	Val	Leu	Leu	Ala	Thr	Leu	Val	Glu	Ala	Ala	Leu	Cys	Ala	Trp	Tyr	690	695	700	
Leu	Met	Ala	Phe	Pro	Pro	Glu	Val	Val	Thr	Asp	Trp	Gln	Val	Leu	Pro	705	710	715	720
Thr	Glu	Val	Leu	Glu	His	Cys	Arg	Met	Arg	Ser	Trp	Val	Ser	Leu	Gly	725	730		735
Leu	Val	His	Ile	Thr	Asn	Ala	Val	Leu	Ala	Phe	Leu	Cys	Phe	Leu	Gly	740	745		750
Thr	Phe	Leu	Val	Gln	Ser	Gln	Pro	Gly	Arg	Tyr	Asn	Arg	Ala	Arg	Gly	755	760	765	
Leu	Thr	Phe	Ala	Met	Leu	Ala	Tyr	Phe	Ile	Ile	Trp	Val	Ser	Phe	Val	770	775	780	

Pro	Leu	Leu	Ala	Asn	Val	Gln	Val	Ala	Tyr	Gln	Pro	Ala	Val	Gln	Met
785					790					795					800
Gly	Ala	Ile	Leu	Phe	Cys	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Phe	His	Leu
				805					810					815	
Pro	Lys	Cys	Tyr	Val	Leu	Leu	Trp	Leu	Pro	Glu	Leu	Asn	Thr	Gln	Glu
			820					825					830		
Phe	Phe	Leu	Gly	Arg	Ser	Pro	Lys	Glu	Ala	Ser	Asp	Gly	Asn	Ser	Gly
		835					840					845			
Ser	Ser	Glu	Ala	Thr	Arg	Gly	His	Ser	Glu						
850						855									